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OM protein - protein search, using sw model

Run on: June 21, 2004, 13:59:37 ; Search time 48 Seconds
(without alignments)
1952.669 Million cell updates/sec

Title: US-10-091-841A-9

Perfect score: 1706

Sequence: 1 MEGSAAPLRTRVCIIGSGP.....ALDAEHVLOEVGAQVGKSDZ 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1706	100.0	332	14	US-10-091-841-9
2	1702	99.8	331	14	Sequence 9, Appl
3	1581	92.7	333	12	Sequence 10, Appl
4	1581	92.7	333	12	Sequence 42556, A
5	1523	89.3	331	12	Sequence 58732, A
6	1469	86.1	310	14	Sequence 27, Appl
7	1346.5	78.9	383	12	Sequence 72, Appl
8	1346.5	78.9	383	14	Sequence 196, Appl
9	1346.5	78.2	383	12	Sequence 105, Appl
10	1334.5	78.2	383	12	Sequence 141, Appl
11	1334.5	78.2	383	12	Sequence 105, Appl
12	1334.5	78.2	383	14	Sequence 150, Appl
13	1334.5	78.2	383	14	Sequence 150, Appl
14	1333.5	78.2	383	12	Sequence 150, Appl
15	1333.5	78.2	383	14	Sequence 150, Appl

16	1332.5	78.1	383	12	US-10-290-072-87
17	1332.5	78.1	383	12	US-10-290-072-132
18	1332.5	78.1	383	14	US-10-141-531-87
19	1332.5	78.1	383	14	US-10-141-531-132
20	1330.5	78.0	383	12	US-10-290-072-186
21	1330.5	78.0	383	14	US-10-141-531-196
22	1326.5	77.8	383	12	US-10-290-072-114
23	1326.5	77.8	383	12	US-10-290-072-159
24	1326.5	77.8	383	12	US-10-290-072-177
25	1326.5	77.8	383	14	US-10-141-531-114
26	1326.5	77.8	383	14	US-10-141-531-159
27	1326.5	77.7	383	14	US-10-141-531-177
28	1325.5	77.7	383	12	US-10-290-072-96
29	1325.5	77.7	383	12	US-10-290-072-123
30	1325.5	77.7	383	12	US-10-290-072-195
31	1325.5	77.7	383	14	US-10-141-531-96
32	1325.5	77.7	383	14	US-10-141-531-123
33	1325.5	77.7	383	14	US-10-141-531-195
34	1324.5	77.6	383	12	US-10-290-072-168
35	1324.5	77.6	383	14	US-10-141-531-168
36	1324	77.6	333	9	US-09-897-898-3
37	1324	77.6	333	9	US-09-897-898-4
38	1324	77.6	333	9	US-09-897-898-14
39	1324	77.6	333	12	US-09-897-425-38
40	1324	77.6	333	12	US-09-897-425-39
41	1324	77.6	333	12	US-09-897-425-49
42	1324	77.6	333	14	US-10-032-201B-11
43	1324	77.6	333	14	US-10-032-201B-13
44	1324	77.6	333	14	US-10-032-201B-23
45	1324	77.6	365	12	US-10-290-072-61

ALIGNMENTS

RESULT 1

US-10-091-841-9
Sequence 9, Application US/10091841
Publication No. US20030150010A1
GENERAL INFORMATION:
APPLICANT: Cho, Myeong-Je
APPLICANT: Del Val, Greg
APPLICANT: Calliau, Maxime
APPLICANT: Lemauz, Peggy G.
APPLICANT: Buchanan, Bob B.
TITLE OF INVENTION: Barley Gene for Thioredoxin and
TITLE OF INVENTION: NADp-Thioredoxin Reductase
FILE REFERENCE: 2001-0701-30
CURRENT APPLICATION NUMBER: US/10/091,841
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: 09/540,014
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 60/127,198
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: US 60/169,162
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 60/177,740
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 60/177,739
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 332
TYPE: PRT
ORGANISM: Hordeum vulgare
US-10-091-841-9

Query Match 100.0%; Score 1706; DB 14; Length 332;
Best Local Similarity 100.0%; Pred. No. 3.8e-164;
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEGSAAPLRTRVCIIGSGPAAHTAAIYAARAEKPVLFEGWANDIAAGGQTTTTTVE 60

Db 1 MEGSAAAPLRTVCIIIGSGPAHAATAIYAARAEKLPVLEFGWANDIAAGGQLTITDVE 60
QY 61 NFGPFTGIMGIDLMDCRAQSVRFCTNIISETVTEVDFSPRPFRVTSSTTVLADTVV 120
Db 61 NFGPFTGIMGIDLMDCRAQSVRFCTNIISETVTEVDFSPRPFRVTSSTTVLADTVV 120
QY 121 ATGAVARRLHPSGSDTYWNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEEGNFLT KYG 180
Db 121 ATGAVARRLHPSGSDTYWNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEEGNFLT KYG 180
QY 181 SQVYIIHRRNTFRASKIMQARALSNPKIQVWMDSEVVEAYGAGGGLAGVKVKNLVTGE 240
Db 181 SQVYIIHRRNTFRASKIMQARALSNPKIQVWMDSEVVEAYGAGGGLAGVKVKNLVTGE 240
QY 241 VSDLOVSGLFFAIGHEPATKFLNGQLEHADGVATKPGSTHTSVGVPFAAGDVQDKKYR 300
Db 241 VSDLOVSGLFFAIGHEPATKFLNGQLEHADGVATKPGSTHTSVGVPFAAGDVQDKKYR 300
QY 301 QAITAAGSGCMAALDAEHYLOEVGAQVGSZDZ 332
Db 301 QAITAAGSGCMAALDAEHYLOEVGAQVGSZDZ 332

RESULT 2

US-10-194-885-10
; Sequence 10, Application US/10194885
; Publication No. US20030135878A1

GENERAL INFORMATION:

; APPLICANT: Wong, J. H.
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH ELEVATED
; TITLE OF INVENTION: THIOREDUXIN LEVELS
; FILE REFERENCE: 41627200800
; CURRENT APPLICATION NUMBER: US/10/194,885
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 60/307,006
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/538,964
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/126,736
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Barley

US-10-194-885-10

Query Match 99.8%; Score 1702; DB 14; Length 331;
Best Local Similarity 100.0%; Pred. No. 9.5e-164;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGSAAAPLRTVCIIIGSGPAHAATAIYAARAEKLPVLEFGWANDIAAGGQLTITDVE 60
Db 1 MEGSAAAPLRTVCIIIGSGPAHAATAIYAARAEKLPVLEFGWANDIAAGGQLTITDVE 60
QY 61 NFGPFTGIMGIDLMDCRAQSVRFCTNIISETVTEVDFSPRPFRVTSSTTVLADTVV 120
Db 61 NFGPFTGIMGIDLMDCRAQSVRFCTNIISETVTEVDFSPRPFRVTSSTTVLADTVV 120
QY 121 ATGAVARRLHPSGSDTYWNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEEGNFLT KYG 180
Db 121 ATGAVARRLHPSGSDTYWNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEEGNFLT KYG 180
QY 181 SQVYIIHRRNTFRASKIMQARALSNPKIQVWMDSEVVEAYGAGGGLAGVKVKNLVTGE 240
Db 181 SQVYIIHRRNTFRASKIMQARALSNPKIQVWMDSEVVEAYGAGGGLAGVKVKNLVTGE 240
QY 241 VSDLOVSGLFFAIGHEPATKFLNGQLEHADGVATKPGSTHTSVGVPFAAGDVQDKKYR 300

Db 241 VSDLOVSGLFFAIGHEPATKFLNGQLEHADGVATKPGSTHTSVGVPFAAGDVQDKKYR 300
QY 301 QAITAAGSGCMAALDAEHYLOEVGAQVGSZDZ 331
Db 301 QAITAAGSGCMAALDAEHYLOEVGAQVGSZDZ 331

RESULT 3

US-10-425-114-42556
; Sequence 42556, Application US/10425114
; Publication No. US20040034888A1

GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 42556
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700336177_FLI.pep

US-10-425-114-42556

Query Match 92.7%; Score 1581; DB 12; Length 333;
Best Local Similarity 91.8%; Pred. No. 1.8e-151;
Matches 304; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 MEGSAAAPLRTVCIIIGSGPAHAATAIYAARAEKLPVLEFGWANDIAAGGQLTITDVE 60
Db 3 MEGSAAAPLRTVCIIIGSGPAHAATAIYAARAEKLPVLEFGWANDIAAGGQLTITDVE 62
QY 61 NFGPFTGIMGIDLMDCRAQSVRFCTNIISETVTEVDFSPRPFRVTSSTTVLADTVV 120
Db 63 NFGPFTGIMGIDLMDCRAQSVRFCTNIISETVTEVDFSPRPFRVTSSTTVLADTVV 122
QY 121 ATGAVARRLHPSGSDTYWNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEEGNFLT KYG 180
Db 123 ATGAVARRLHPSGSDTYWNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEEGNFLT KYG 182
QY 181 SQVYIIHRRNTFRASKIMQARALSNPKIQVWMDSEVVEAYGAGGGLAGVKVKNLVTGE 240
Db 183 SHVYIIHRRNTFRASKIMQARALSNPKIQVWMDSEVVEAYGAGGGLAGVKVKNLVTGE 242
QY 241 VSDLOVSGLFFAIGHEPATKFLNGQLEHADGVATKPGSTHTSVGVPFAAGDVQDKKYR 300
Db 243 VSDLOVSGLFFAIGHEPATKFLNGQLEHADGVATKPGSTHTSVGVPFAAGDVQDKKYR 302
QY 301 QAITAAGSGCMAALDAEHYLOEVGAQVGSZDZ 331
Db 303 QAITAAGSGCMAALDAEHYLOEVGAQVGSZDZ 333

RESULT 4

US-10-425-114-58732
; Sequence 58732, Application US/10425114
; Publication No. US20040034888A1

GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei

;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

;; FILE REFERENCE: 38-21(53313)B
;; CURRENT APPLICATION NUMBER: US/10/425,114

;; CURRENT FILING DATE: 2003-04-28

;; NUMBER OF SEQ ID NOS: 73128

;; SEQ ID NO 58732

;; LENGTH: 333

;; TYPE: PRT

;; ORGANISM: Zea mays

;; FEATURE:

;; OTHER INFORMATION: Clone ID: 700447274_FLI.pcp

US-10-425-114-58732

Query Match 92.7%; Score 1581; DB 12; Length 333;

Best Local Similarity 91.8%; Pred. No. 1.8e-151;

Matches 304; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 MEGSAAPLRTRVCIIGSGPAHAHTAAIYAARAEKLPVLFEQWANDIAAGGQTTTTTIVE 60

DB 3 MEGSAAPLRTRVCIIGSGPAHAHTAAIYAARAEKLPVLFEQWANDIAAGGQTTTTTIVE 62

QY 61 NFPGPTGIMGIDLMDNCRAQSVFSGTNISETVTEVDFSAARPRVTSSTTVLADTVV 120

DB 63 NFPGPTGIMGIDLMDNCRAQSVFSGTNISETVTEVDFSAARPRVTSSTTVLADTVV 122

QY 121 ATGAVARLHFGSDTYNNRGISACVCDGAAPFRNKPIAVIGGDSAMEEGNFLTXYG 180

DB 123 ATGAVARLHFGSDTYNNRGISACVCDGAAPFRNKPIAVIGGDSAMEEGNFLTXYG 182

QY 181 SOVYIIHRRNTFRASKIMQARALSNPKIQVWVDSVVEAYGAGGGPLAGVKVKNLVTGE 240

DB 183 SHVYIIHRRNTFRASKIMQARALSNPKIQVWVDSVVEAYGAGGGPLAGVKVKNLVTGE 242

QY 241 VSDLOVSGLFFAIGHEPATKFLNGOLEHADGVYATKPGSTHTSVGVEFAAGDVQDKKYR 300

DB 243 VSDLOVSGLFFAIGHEPATKFLNGOLEHADGVYATKPGSTHTSVGVEFAAGDVQDKKYR 302

QY 301 QAITAAGSGCMAALDAEHLQEVGAQVCKSD 331

DB 303 QAITAAGSGCMAALDAEHLQEVGAQVCKSD 333

RESULT 5

US-10-194-885-11

;; Sequence 11, Application US/10194885

;; Publication No. US20030135878A1

;; GENERAL INFORMATION:

;; APPLICANT: Wong, J. H.

;; APPLICANT: Cho, Myeong-Je

;; APPLICANT: Lemaux, Peggy G.

;; APPLICANT: Buchanan, Bob

;; TITLE OF INVENTION: TRANSGENIC PLANTS WITH ELEVATED

;; TITLE OF INVENTION: THIOREDUXIN LEVELS

;; FILE REFERENCE: 416272000800

;; CURRENT APPLICATION NUMBER: US/10/194,885

;; CURRENT FILING DATE: 2002-07-12

;; PRIOR APPLICATION NUMBER: 60/307,006

;; PRIOR FILING DATE: 2001-07-19

;; PRIOR APPLICATION NUMBER: 09/538,864

;; PRIOR FILING DATE: 2000-03-29

;; PRIOR APPLICATION NUMBER: 60/126,736

;; PRIOR FILING DATE: 1999-03-29

;; NUMBER OF SEQ ID NOS: 55

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 11

;; LENGTH: 331

;; TYPE: PRT

;; ORGANISM: wheat

US-10-194-885-11

Query Match

Best Local Similarity

89.3%; Score 1523; DB 14; Length 331;

87.9%; Pred. No. 1.3e-145;

Matches 291; Conservative 20; Mismatches 20; Indels 0; Gaps 0;

QY 1 MEGSAAPLRTRVCIIGSGPAHAHTAAIYAARAEKLPVLFEQWANDIAAGGQTTTTTIVE 60

DB 1 MEGSAAPLRTRVCIIGSGPAHAHTAAIYAARAEKLPVLFEQWANDIAAGGQTTTTTIVE 60

QY 61 NFPGPTGIMGIDLMDNCRAQSVFSGTNISETVTEVDFSAARPRVTSSTTVLADTVV 120

DB 61 NFPGPTGIMGIDLMDNCRAQSVFSGTNISETVTEVDFSAARPRVTSSTTVLADTVV 120

QY 121 ATGAVARLHFGSDTYNNRGISACVCDGAAPFRNKPIAVIGGDSAMEEGNFLTXYG 180

DB 121 ATGAVARLHFGSDTYNNRGISACVCDGAAPFRNKPIAVIGGDSAMEEGNFLTXYG 180

QY 181 SOVYIIHRRNTFRASKIMQARALSNPKIQVWVDSVVEAYGAGGGPLAGVKVKNLVTGE 240

DB 181 SRVYIIHRRNTFRASKIMQARALSNPKIQVWVDSVVEAYGAGGGPLAGVKVKNLVTGE 240

QY 241 VSDLOVSGLFFAIGHEPATKFLNGOLEHADGVYATKPGSTHTSVGVEFAAGDVQDKKYR 300

DB 241 VSDLOVSGLFFAIGHEPATKFLNGOLEHADGVYATKPGSTHTSVGVEFAAGDVQDKKYR 300

QY 301 QAITAAGSGCMAALDAEHLQEVGAQVCKSD 331

DB 301 QAITAAGSGCMAALDAEHLQEVGAQVCKSD 331

RESULT 6

US-10-306-292-27

;; Sequence 27, Application US/10306292

;; Publication No. US20030145347A1

;; GENERAL INFORMATION:

;; APPLICANT: Lananan, Michael B.

;; APPLICANT: Dessai, Nalini M.

;; APPLICANT: Gasdaska, Pamela Y.

;; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL

;; TITLE OF INVENTION: THEREIN

;; FILE REFERENCE: A-31383P1

;; CURRENT APPLICATION NUMBER: US/10/306,292

;; CURRENT FILING DATE: 2002-11-27

;; PRIOR APPLICATION NUMBER: US/09/598,747

;; PRIOR FILING DATE: 2000-06-21

;; NUMBER OF SEQ ID NOS: 42

;; SOFTWARE: PatentIn Ver. 2.1

;; SEQ ID NO 27

;; LENGTH: 310

;; TYPE: PRT

;; ORGANISM: Oryza sativa

US-10-306-292-27

Query Match 86.1%; Score 1469; DB 14; Length 310;

Best Local Similarity 91.6%; Pred. No. 3.6e-140;

Matches 283; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 1 MEGSAAPLRTRVCIIGSGPAHAHTAAIYAARAEKLPVLFEQWANDIAAGGQTTTTTIVE 60

DB 1 MEGSAAPLRTRVCIIGSGPAHAHTAAIYAARAEKLPVLFEQWANDIAAGGQTTTTTIVE 60

QY 61 NFPGPTGIMGIDLMDNCRAQSVFSGTNISETVTEVDFSAARPRVTSSTTVLADTVV 120

DB 61 NFPGPTGIMGIDLMDNCRAQSVFSGTNISETVTEVDFSAARPRVTSSTTVLADTVV 120

QY 121 ATGAVARLHFGSDTYNNRGISACVCDGAAPFRNKPIAVIGGDSAMEEGNFLTXYG 180

DB 121 ATGAVARLHFGSDTYNNRGISACVCDGAAPFRNKPIAVIGGDSAMEEGNFLTXYG 180

QY 181 SOVYIIHRRNTFRASKIMQARALSNPKIQVWVDSVVEAYGAGGGPLAGVKVKNLVTGE 240

DB 181 SHVYIIHRRNTFRASKIMQARALSNPKIQVWVDSVVEAYGAGGGPLAGVKVKNLVTGE 240

QY 241 VSDLOVSGLFFAIGHEPATKFLNGOLEHADGVYATKPGSTHTSVGVEFAAGDVQDKKYR 300

DB 241 VSDLOVSGLFFAIGHEPATKFLNGOLEHADGVYATKPGSTHTSVGVEFAAGDVQDKKYR 300

Qy 301 QAITAAGSG 309
 Db 301 QAITAAGSG 309

RESULT 7

US-10-290-072-72
 ; Sequence 72, Application US/10290072
 ; Publication No. US2003021151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Dalmia, Bipin K.
 ; APPLICANT: Desjarlais, John R.
 ; APPLICANT: Heifetz, Peter
 ; APPLICANT: Lugimbuhl, Peter
 ; APPLICANT: Muchhal, Umesh
 ; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
 ; FILE REFERENCE: A-71457-3
 ; CURRENT APPLICATION NUMBER: US/10/290,072
 ; CURRENT FILING DATE: 2002-11-06
 ; PRIOR APPLICATION NUMBER: US 60/370,609
 ; PRIOR FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: US 60/376,682
 ; PRIOR FILING DATE: 2002-04-29
 ; PRIOR APPLICATION NUMBER: US 10/141,531
 ; PRIOR FILING DATE: 2002-05-06
 ; PRIOR APPLICATION NUMBER: US 60/289,029
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 239
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 72
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-10-290-072-72

Query Match 78.9%; Score 1346.5; DB 12; Length 383;
 Best Local Similarity 76.6%; Pred. No. 1.3e-127;
 Matches 258; Conservative 39; Mismatches 31; Indels 9; Gaps 2;
 Qy 4 SAAAPL-----RTRVCIIGSGPAAHTAAIYAARAELKPVLFEGWMANDIAAGGQLTITTD 58
 Db 47 SAAAADMETHKTKVICVSGSPAAHTAAIYASRAELKPLLFEQWMANDIAPGGQLTITTD 106
 Qy 59 VENPFGPTGIMGIDLMNCRAQSVRFGNLSLSEVTEVDPSARPPRVTSSTTVLADTV 118
 Db 107 VENPFGPPEGILGIDIVERFKQSERFGTITFTETVNVKVDPSFKPKLFTDSRTVLADSV 166
 Qy 119 VVATGAVARELHPSGSDT----YNNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEEGN 174
 Db 167 IISTGAVAKLSFTSGEGNGGFWNRGISACAVCDGAAPIFRNKPLVVGSGDSAMEEAN 226
 Qy 175 FLTKYGSQVYIIHRRNTFRASKIMQARALSNPKIQVWDSVEVYAGGAGGGLAGVKVK 234
 Db 227 FLTKYGSQVYIIHRRDTFRASKIMQARALSNPKIEVIMNSAVVEAYGDENGRVLGGLVKV 286
 Qy 235 NLVTGVSQVSDLOVSGLFFAIGHEPATKFLNGQLELHADGVYATKPGSTHTSVGVFAAGDV 294
 Db 287 NVVTGVSQVSDLVKVSGLFFAIGHEPATKFLNGQLELDEDDGVYVTKPGTITKTSVGVFAAGDV 346
 Qy 295 QDKKYRQAITAAGSGCMAALDAEHYLOEYGAQVKGSD 331
 Db 347 QDKKYRQAITAAGTGCMAALDAEHYLOEYGSQEGKSD 383

RESULT 8

US-10-141-531-72
 ; Sequence 72, Application US/10141531
 ; Publication No. US20030100743A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Briggs, Steven P.

APPLICANT: Dalmia, Bipin K.
 APPLICANT: del Val, Greg
 APPLICANT: Desjarlais, John R.
 APPLICANT: Heifetz, Peter
 APPLICANT: Lugimbuhl, Peter
 APPLICANT: Muchhal, Umesh
 TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
 FILE REFERENCE: A-71457-2/RET/BMS/BMK
 CURRENT APPLICATION NUMBER: US/10/141,531
 CURRENT FILING DATE: 2002-05-06
 PRIOR APPLICATION NUMBER: US 60/370,609
 PRIOR FILING DATE: 2002-04-05
 PRIOR APPLICATION NUMBER: US 60/289,029
 PRIOR FILING DATE: 2001-05-04
 NUMBER OF SEQ ID NOS: 208
 SOFTWARE: Patent in version 3.1
 SEQ ID NO 72
 LENGTH: 383
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 US-10-141-531-72

Query Match 78.9%; Score 1346.5; DB 14; Length 383;
 Best Local Similarity 76.6%; Pred. No. 1.3e-127;
 Matches 258; Conservative 39; Mismatches 31; Indels 9; Gaps 2;
 Qy 4 SAAAPL-----RTRVCIIGSGPAAHTAAIYAARAELKPVLFEGWMANDIAAGGQLTITTD 58
 Db 47 SAAAADMETHKTKVICVSGSPAAHTAAIYASRAELKPLLFEQWMANDIAPGGQLTITTD 106
 Qy 59 VENPFGPTGIMGIDLMNCRAQSVRFGNLSLSEVTEVDPSARPPRVTSSTTVLADTV 118
 Db 107 VENPFGPPEGILGIDIVERFKQSERFGTITFTETVNVKVDPSFKPKLFTDSRTVLADSV 166
 Qy 119 VVATGAVARELHPSGSDT----YNNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEEGN 174
 Db 167 IISTGAVAKLSFTSGEGNGGFWNRGISACAVCDGAAPIFRNKPLVVGSGDSAMEEAN 226
 Qy 175 FLTKYGSQVYIIHRRNTFRASKIMQARALSNPKIQVWDSVEVYAGGAGGGLAGVKVK 234
 Db 227 FLTKYGSQVYIIHRRDTFRASKIMQARALSNPKIEVIMNSAVVEAYGDENGRVLGGLVKV 286
 Qy 235 NLVTGVSQVSDLOVSGLFFAIGHEPATKFLNGQLELHADGVYATKPGSTHTSVGVFAAGDV 294
 Db 287 NVVTGVSQVSDLVKVSGLFFAIGHEPATKFLNGQLELDEDDGVYVTKPGTITKTSVGVFAAGDV 346
 Qy 295 QDKKYRQAITAAGSGCMAALDAEHYLOEYGAQVKGSD 331
 Db 347 QDKKYRQAITAAGTGCMAALDAEHYLOEYGSQEGKSD 383

RESULT 9

US-10-032-201B-196
 ; Sequence 196, Application US/10032201B
 ; Publication No. US20030167524A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Rooijen, Gijb
 ; APPLICANT: Deckers, Harm
 ; APPLICANT: Heifetz, Peter Bernard
 ; APPLICANT: Briggs, Steven
 ; APPLICANT: Dalmia, Bipin Kumar
 ; APPLICANT: del Val, Greg
 ; APPLICANT: Moloney, Maurice
 ; APPLICANT: Zaplachinski, Steve
 TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
 FILE REFERENCE: 38814 351B
 CURRENT APPLICATION NUMBER: US/10/032,201B
 CURRENT FILING DATE: 2001-12-19
 NUMBER OF SEQ ID NOS: 313
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 196
 LENGTH: 383

TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-032-201B-196

Query Match 78.9%; Score 1346.5; DB 14; Length 383;
Best Local Similarity 76.6%; Pred. No. 1.3e-127;
Matches 258; Conservative 39; Mismatches 31; Indels 9; Gaps 2;

QY 4 SAAAPL-----RTRVCIIGSGPAAHTAAIYAARAEKLPVLFEQWANDIAAGGQLTITTD 58
DB 47 SAAAVDMETHKTKVCIIVGSGPAAHTAAIYASRAELKPLFEQWANDIAAGGQLTITTD 106
QY 59 VENPFGPPTGIMGIDLDNCRQAQSVRFGTNILSETVTEVDFSAARPRVTSDSTTVLADTV 118
DB 107 VENPFGPPTGIMGIDLDNCRQAQSVRFGTNILSETVTEVDFSAARPRVTSDSTTVLADTV 166
QY 119 VVATGAVARRLHFGSDT-----YNNRGISACAVCDGAAPFRNKPIAVIGGSDSAMEEGN 174
DB 167 IISTGAVAKRLSFTGSGEGNGGFWNRGISACAVCDGAAPFRNKPLVVIIGGSDSAMEEGN 226
QY 175 FLTKYGSQVYIHRNTFRASKIMQARALSNPKIOVWDSVVEAYGGAGGGLAGVKVK 234
DB 227 FLTKYGSQVYIHRNTFRASKIMQARALSNPKIOVWDSVVEAYGGAGGGLAGVKVK 286
QY 235 NLVTGEVSDLVQSGLFFAIGHEPATKFLNGQLHLDAGYVATKPGSTHTSVEGVFAAGDV 294
DB 287 NVVTGDSVLDKVSGLFFAIGHEPATKFLDQGLDDEDEGYVTKPGTTKTSVGVFAAGDV 346
QY 295 QDKYRQAITAAGSGCMAALDAEHYLOEVGAQVQKSD 331
DB 347 QDKYRQAITAAGSGCMAALDAEHYLOEIGSQEGKSD 383

RESULT 10

US-10-290-072-105
Sequence 105, Application US/10290072
Publication No. US20030211511A1

GENERAL INFORMATION:

APPLICANT: Briggs, Steven P.
APPLICANT: Daimia, Bipin K.
APPLICANT: Del Val, Greg
APPLICANT: Desjarlais, John R.
APPLICANT: Heifetz, Peter
APPLICANT: Luginbuhl, Peter
APPLICANT: Muchhal, Umesh
TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
FILE REFERENCE: A-71457-3
CURRENT APPLICATION NUMBER: US/10/290,072
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: US 60/370,609
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/376,682
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 10/141,531
PRIOR FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US 60/289,029
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 239
SOFTWARE: Patentin version 3.2
SEQ ID NO 105
LENGTH: 383
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Arabidopsis thaliana variant
US-10-290-072-105

Query Match 78.2%; Score 1334.5; DB 12; Length 383;
Best Local Similarity 76.0%; Pred. No. 2.1e-126;
Matches 256; Conservative 39; Mismatches 33; Indels 9; Gaps 2;

QY 4 SAAAPL-----RTRVCIIGSGPAAHTAAIYAARAEKLPVLFEQWANDIAAGGQLTITTD 58
DB 47 SAAAVDMETHKTKVCIIVGSGPAAHTAAIYASRAELKPLFEQWANDIAAGGQLTITTD 106
QY 59 VENPFGPPTGIMGIDLDNCRQAQSVRFGTNILSETVTEVDFSAARPRVTSDSTTVLADTV 118
DB 107 VENPFGPPTGIMGIDLDNCRQAQSVRFGTNILSETVTEVDFSAARPRVTSDSTTVLADTV 166
QY 119 VVATGAVARRLHFGSDT-----YNNRGISACAVCDGAAPFRNKPIAVIGGSDSAMEEGN 174
DB 167 IISTGAVAKRLSFTGSGEGNGGFWNRGISACAVCDGAAPFRNKPLVVIIGGSDSAMEEGN 226

DB 47 SAAAVDMETHKTKVCIIVGSGPAAHTAAIYASRAELKPLFEQWANDIAAGGQLTITTD 106
QY 59 VENPFGPPTGIMGIDLDNCRQAQSVRFGTNILSETVTEVDFSAARPRVTSDSTTVLADTV 118
DB 107 VENPFGPPTGIMGIDLDNCRQAQSVRFGTNILSETVTEVDFSAARPRVTSDSTTVLADTV 166
QY 119 VVATGAVARRLHFGSDT-----YNNRGISACAVCDGAAPFRNKPIAVIGGSDSAMEEGN 174
DB 167 IISTGAVAKRLSFTGSGEGNGGFWNRGISACAVCDGAAPFRNKPLVVIIGGSDSAMEEGN 226
QY 175 FLTKYGSQVYIHRNTFRASKIMQARALSNPKIOVWDSVVEAYGGAGGGLAGVKVK 234
DB 227 FLTKYGSQVYIHRNTFRASKIMQARALSNPKIOVWDSVVEAYGGAGGGLAGVKVK 286
QY 235 NLVTGEVSDLVQSGLFFAIGHEPATKFLNGQLHLDAGYVATKPGSTHTSVEGVFAAGDV 294
DB 287 NVVTGDSVLDKVSGLFFAIGHEPATKFLDQGLDDEDEGYVTKPGTTKTSVGVFAAGDV 346
QY 295 QDKYRQAITAAGSGCMAALDAEHYLOEVGAQVQKSD 331
DB 347 QDKYRQAITAAGSGCMAALDAEHYLOEIGSQEGKSD 383

RESULT 11

US-10-290-072-141
Sequence 141, Application US/10290072
Publication No. US20030211511A1

GENERAL INFORMATION:

APPLICANT: Briggs, Steven P.
APPLICANT: Daimia, Bipin K.
APPLICANT: Del Val, Greg
APPLICANT: Desjarlais, John R.
APPLICANT: Heifetz, Peter
APPLICANT: Luginbuhl, Peter
APPLICANT: Muchhal, Umesh
TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
FILE REFERENCE: A-71457-3
CURRENT APPLICATION NUMBER: US/10/290,072
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: US 60/370,609
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/376,682
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 10/141,531
PRIOR FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US 60/289,029
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 239
SOFTWARE: Patentin version 3.2
SEQ ID NO 141
LENGTH: 383
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Arabidopsis thaliana variant
US-10-290-072-141

Query Match 78.2%; Score 1334.5; DB 12; Length 383;
Best Local Similarity 76.0%; Pred. No. 2.1e-126;
Matches 256; Conservative 39; Mismatches 33; Indels 9; Gaps 2;

QY 4 SAAAPL-----RTRVCIIGSGPAAHTAAIYAARAEKLPVLFEQWANDIAAGGQLTITTD 58
DB 47 SAAAVDMETHKTKVCIIVGSGPAAHTAAIYASRAELKPLFEQWANDIAAGGQLTITTD 106
QY 59 VENPFGPPTGIMGIDLDNCRQAQSVRFGTNILSETVTEVDFSAARPRVTSDSTTVLADTV 118
DB 107 VENPFGPPTGIMGIDLDNCRQAQSVRFGTNILSETVTEVDFSAARPRVTSDSTTVLADTV 166
QY 119 VVATGAVARRLHFGSDT-----YNNRGISACAVCDGAAPFRNKPIAVIGGSDSAMEEGN 174
DB 167 IISTGAVAKRLSFTGSGEGNGGFWNRGISACAVCDGAAPFRNKPLVVIIGGSDSAMEEGN 226

QY 175 FLTKYGSQVYIIHRRNTFRASKINQARALSNPKIQVWDSVEVYAGGGGGLAGVKV 234
DB 227 FLTKYGSQVYIIHRRNTFRASKINQARALSNPKIQVWDSVEVYAGGGGGLAGVKV 286
QY 235 NLVTGEVSDLVQSGLPFAIGHEPATKFLNGQLEHADGYVATKPGSTHRSVEGVFAAGDV 294
DB 287 NVVTGVDVSLKVSGLPFAIGHEPATKFLNGQLEHADGYVATKPGSTHRSVEGVFAAGDV 346
QY 295 QDKYRQAITAAGSGCMAALDAEHLQEVGAQVKGSD 331
DB 347 QDKYRQAITAAGSGCMAALDAEHLQEVGAQVKGSD 383

RESULT 12

US-10-141-531-105
; Sequence 105, Application US/10141531
; Publication No. US20030100743A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Lugimbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-2/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/141,531
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 105
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Arabidopsis thaliana variant
US-10-141-531-105

Query Match 78.2%; Score 1334.5; DB 14; Length 383;
Best Local Similarity 76.0%; Pred. No. 2.1e-126;
Matches 256; Conservative 39; Mismatches 33; Indels 9; Gaps 2;

QY 4 SAAAPL-----RTRVCIIGSGPAAHTAAIYAARAEKPLVLEFGWMANDIAAGGQTTTTD 58
DB 47 SAAAVDMETHKTKVCIIVSGPAAHTAAIYASRAELKPLLEFGWMANDIAAGGQTTTTD 106
QY 59 VENFPFGPTGIMGIDLMNCRAQSVREGTNISETVTEVDFSPARFRTSDSTTVLADTV 118
DB 107 VENFPFGPEGLIGDIVEKFRKQSERFGTTITFTVKNKVDFFSKPKFLTDSRTVLADSV 166
QY 119 VVATGAVARLHFGSGDT----YNNRGISACVCDGAAPIFRNKPIAVIGGDSAMEGN 174
DB 167 IISTGAVAKLSFTSGEGGFWNRGISACVCDGAAPIFRNKPLVWIGGDSAMEAN 226
QY 175 FLTKYGSQVYIIHRRNTFRASKINQARALSNPKIQVWDSVEVYAGGGGGLAGVKV 234
DB 287 NVVTGVDVSLKVSGLPFAIGHEPATKFLNGQLEHADGYVATKPGSTHRSVEGVFAAGDV 346
QY 295 QDKYRQAITAAGSGCMAALDAEHLQEVGAQVKGSD 331
DB 347 QDKYRQAITAAGSGCMAALDAEHLQEVGAQVKGSD 383

RESULT 13

US-10-290-072-150
; Sequence 150, Application US/10290072
; Publication No. US20030211511A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Lugimbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-3
; CURRENT APPLICATION NUMBER: US/10/290,072

US-10-141-531-141
; Sequence 141, Application US/10141531
; Publication No. US20030100743A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Lugimbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-2/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/141,531
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 141
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Arabidopsis thaliana variant
US-10-141-531-141

Query Match 78.2%; Score 1334.5; DB 14; Length 383;
Best Local Similarity 76.0%; Pred. No. 2.1e-126;
Matches 256; Conservative 39; Mismatches 33; Indels 9; Gaps 2;
QY 4 SAAAPL-----RTRVCIIGSGPAAHTAAIYAARAEKPLVLEFGWMANDIAAGGQTTTTD 58
DB 47 SAAAVDMETHKTKVCIIVSGPAAHTAAIYASRAELKPLLEFGWMANDIAAGGQTTTTD 106
QY 59 VENFPFGPTGIMGIDLMNCRAQSVREGTNISETVTEVDFSPARFRTSDSTTVLADTV 118
DB 107 VENFPFGPEGLIGDIVEKFRKQSERFGTTITFTVKNKVDFFSKPKFLTDSRTVLADSV 166
QY 119 VVATGAVARLHFGSGDT----YNNRGISACVCDGAAPIFRNKPIAVIGGDSAMEGN 174
DB 167 IISTGAVAKLSFTSGEGGFWNRGISACVCDGAAPIFRNKPLVWIGGDSAMEAN 226
QY 175 FLTKYGSQVYIIHRRNTFRASKINQARALSNPKIQVWDSVEVYAGGGGGLAGVKV 234
DB 287 NVVTGVDVSLKVSGLPFAIGHEPATKFLNGQLEHADGYVATKPGSTHRSVEGVFAAGDV 286
QY 235 NLVTGEVSDLVQSGLPFAIGHEPATKFLNGQLEHADGYVATKPGSTHRSVEGVFAAGDV 294
DB 287 NVVTGVDVSLKVSGLPFAIGHEPATKFLNGQLEHADGYVATKPGSTHRSVEGVFAAGDV 346
QY 295 QDKYRQAITAAGSGCMAALDAEHLQEVGAQVKGSD 331
DB 347 QDKYRQAITAAGSGCMAALDAEHLQEVGAQVKGSD 383

RESULT 14

US-10-290-072-150
; Sequence 150, Application US/10290072
; Publication No. US20030211511A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Lugimbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-3
; CURRENT APPLICATION NUMBER: US/10/290,072

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; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/376,682
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 10/141,531
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 150
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Arabidopsis thaliana variant
US-10-290-072-150

```

```

Query Match      78.2%; Score 1333.5; DB 12; Length 383;
Best Local Similarity 76.0%; Pred. No. 2.7e-126;
Matches 256; Conservative 39; Mismatches 33; Indels 9; Gaps 2;

QY      4 SAAAPL-----RFRVCIIGSGPAAHTAAIYAARAEKPVLFEGWMANDIAAGGQLTITTD 58
      47 SAAAAVDMMETHKTKVCIVGSGPAAHTAAIYASRAELKPLLFEGWMANDIAAGGQLTITTD 106
QY      59 VENFPFGPTGIMGIDLMDNCRAQSFRFGTNIILSETVTEVDFSGARPPRVTSSTTVLADTV 118
      107 VENFPFGPEGLIGDIVEKFKQSERFGTITFTETVNVKVDFFSKPKFLFTDSRTVLADSV 166
QY      119 VVATGAVARLHFSGSDT-----YVNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEBN 174
      167 IISTGAVAKRLSFTGSGEGNGGFVNRGISACAVCDGAAPIFRNKPLVVIIGGDSAMEBAN 226
QY      175 FLTKYGSOVYIIHRRNTFRASKIMOARALSNPKIQVWVDSVVEAYGAGGGLAGVKVK 234
      227 FLTKYGSKVYIIHRFTFNASKIMOARALSNPKIEVWNSAVVEAYGDENGRVLGGLVKV 286
QY      235 NLVTGEVSDLOVSGLFFAIGHPEPATKFLNGQLELHADGYVATKPGSTHTSVGVFAAGDV 294
      287 NVVTGVDVSDLKVSGLFFAIGHPEPATKFLDQGLDELDGYVTKPGTKTSVVGVAAGDV 346
QY      295 QDKKYRQAITAAGSGCMAALDAEHYLOEVGAQVGKSD 331
      347 QDKKYRQAITAAGTGCMAALDAEHYLOEIGSQEGKSD 383

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RESULT 15
US-10-141-531-150
; Sequence 150, Application US/10141531
; Publication No. US20030100743A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Laginbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioresdoxin Reductase Activity
; FILE REFERENCE: A-71457-2/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/141,531
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 150
; LENGTH: 383
; TYPE: PRT

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; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Arabidopsis thaliana variant
US-10-141-531-150

Query Match      78.2%; Score 1333.5; DB 14; Length 383;
Best Local Similarity 76.0%; Pred. No. 2.7e-126;
Matches 256; Conservative 39; Mismatches 33; Indels 9; Gaps 2;

QY      4 SAAAPL-----RFRVCIIGSGPAAHTAAIYAARAEKPVLFEGWMANDIAAGGQLTITTD 58
      47 SAAAAVDMMETHKTKVCIVGSGPAAHTAAIYASRAELKPLLFEGWMANDIAAGGQLTITTD 106
QY      59 VENFPFGPTGIMGIDLMDNCRAQSFRFGTNIILSETVTEVDFSGARPPRVTSSTTVLADTV 118
      107 VENFPFGPEGLIGDIVEKFKQSERFGTITFTETVNVKVDFFSKPKFLFTDSRTVLADSV 166
QY      119 VVATGAVARLHFSGSDT-----YVNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEBN 174
      167 IISTGAVAKRLSFTGSGEGNGGFVNRGISACAVCDGAAPIFRNKPLVVIIGGDSAMEBAN 226
QY      175 FLTKYGSOVYIIHRRNTFRASKIMOARALSNPKIQVWVDSVVEAYGAGGGLAGVKVK 234
      227 FLTKYGSKVYIIHRFTFNASKIMOARALSNPKIEVWNSAVVEAYGDENGRVLGGLVKV 286
QY      235 NLVTGEVSDLOVSGLFFAIGHPEPATKFLNGQLELHADGYVATKPGSTHTSVGVFAAGDV 294
      287 NVVTGVDVSDLKVSGLFFAIGHPEPATKFLDQGLDELDGYVTKPGTKTSVVGVAAGDV 346
QY      295 QDKKYRQAITAAGSGCMAALDAEHYLOEVGAQVGKSD 331
      347 QDKKYRQAITAAGTGCMAALDAEHYLOEIGSQEGKSD 383

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Search completed: June 21, 2004, 14:07:39
Job time : 49 secs

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OM protein - protein search, using sw model

Run on: June 21, 2004, 13:45:47 ; Search time 22 Seconds
(without alignments)
779.083 Million cell updates/sec

Title: US-10-091-841A-9

Perfect score: 1706

Sequence: 1 MEGSAAAPLRTVCIIGSGP.....ALDAHYLQEVGAQVKSDZ 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Issued Patents AA:*
- 2: /cgm2_6/ptodata/2/iaa/5A COMB.pdp:*
- 3: /cgm2_6/ptodata/2/iaa/5B COMB.pdp:*
- 4: /cgm2_6/ptodata/2/iaa/6A COMB.pdp:*
- 5: /cgm2_6/ptodata/2/iaa/6B COMB.pdp:*
- 6: /cgm2_6/ptodata/2/iaa/PCTUS COMB.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1706	100.0	332	4	US-09-540-014-9
2	1469	86.1	310	4	US-09-598-747-27
3	1296	76.0	333	4	US-09-598-747-25
4	1250.5	73.3	332	4	US-09-540-014-24
5	948	55.6	334	1	US-08-386-729A-7
6	910.5	53.4	311	4	US-09-198-452A-331
7	707.5	41.5	320	4	US-09-328-352-5678
8	697.5	40.9	317	4	US-09-328-352-8114
9	688	40.3	349	4	US-09-489-039A-12096
10	684.5	40.1	339	4	US-09-543-681A-5633
11	677	39.7	323	4	US-09-252-991A-29849
12	674	39.5	321	4	US-09-540-014-25
13	542.5	31.8	310	4	US-09-134-000C-5514
14	458	26.8	329	4	US-09-134-000C-3897
15	410.5	24.1	300	4	US-09-598-747-7
16	401.5	23.5	508	4	US-09-134-001C-4570
17	400.5	23.5	215	4	US-09-252-991A-31700
18	397.5	23.3	538	4	US-09-543-681A-4490
19	382.5	22.4	253	4	US-09-134-001C-5512
20	373.5	21.9	510	1	US-08-220-677A-2
21	369.5	21.7	523	4	US-09-328-352-6394
22	369.5	21.7	523	4	US-09-328-352-6395
23	368.5	21.6	512	4	US-09-107-532A-6559
24	365	21.4	301	4	US-09-598-747-6
25	350.5	20.5	522	4	US-09-252-991A-28463
26	323	18.9	524	4	US-09-540-236-2706
27	316.5	18.6	199	4	US-09-252-991A-31441

28	266.5	15.6	192	4	US-09-489-039A-13402	Sequence 13402, A
29	252.5	14.8	339	4	US-09-107-532A-6420	Sequence 6420, Ap
30	197	11.5	334	4	US-09-134-000C-5068	Sequence 5068, Ap
31	180.5	10.6	478	4	US-09-134-000C-5543	Sequence 5543, Ap
32	164.5	9.6	474	4	US-09-556-877-90	Sequence 90, Appl
33	164.5	9.6	474	4	US-09-620-412C-90	Sequence 90, Appl
34	164.5	9.6	474	4	US-09-410-568-90	Sequence 90, Appl
35	164.5	9.6	474	4	US-09-598-419-90	Sequence 90, Appl
36	154	9.0	87	4	US-09-134-001C-5497	Sequence 5497, Ap
37	151	8.9	474	4	US-09-328-352-7757	Sequence 7757, Ap
38	151	8.9	496	4	US-09-328-352-6168	Sequence 6168, Ap
39	150	8.8	564	2	US-08-878-957-32	Sequence 32, Appl
40	150	8.8	581	4	US-09-489-039A-11496	Sequence 11496, A
41	149.5	8.8	491	4	US-09-262-856A-5	Sequence 5, Appl
42	147	8.6	564	1	US-08-427-097-2	Sequence 2, Appl
43	147	8.6	564	1	US-08-427-097-14	Sequence 14, Appl
44	147	8.6	564	1	US-08-427-097-16	Sequence 16, Appl
45	147	8.6	564	1	US-08-427-097-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

```

US-09-540-014-9
; Sequence 9, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillau, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; TITLE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-540-014-9

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Query Match	100.0%;	Score 1706;	DB 4;	Length 332;
Best Local Similarity	100.0%;	Pred. No. 1.1e-179;	Indels 0;	Gaps 0;
Matches 332;	Conservative 0;	Mismatches 0;		
Qv	1	MEGSAAAPLRTVCIIGSGPAHTAAIYAARAEKPVLPFGWMANDIAAGGQTTTDDVE	60	
Db	1	MEGSAAAPLRTVCIIGSGPAHTAAIYAARAEKPVLPFGWMANDIAAGGQTTTDDVE	60	
Qv	61	NFGPPTGIGIDIMDNCRACQSVFCNIISETVTEVDSARFRTVSDSTTVLADTVV	120	
Db	61	NFGPPTGIGIDIMDNCRACQSVFCNIISETVTEVDSARFRTVSDSTTVLADTVV	120	
Qv	121	ATGAVARLHFSGSDTYWNRGISACAVCDGAAPIFRNKPIAVTGGDSAMEEGNFTKYG	180	
Db	121	ATGAVARLHFSGSDTYWNRGISACAVCDGAAPIFRNKPIAVTGGDSAMEEGNFTKYG	180	
Qv	181	SOVYIIHRRNTFRASKTMOARALSNPKIQVWDSVEVYAGGGGGLAGYKKNLTG	240	
Db	181	SOVYIIHRRNTFRASKTMOARALSNPKIQVWDSVEVYAGGGGGLAGYKKNLTG	240	

QY 241 VSDLOVSGLFFAIGHEPATKFLNGOLELHADGYVATKPGSTHTSVEGVFAAGDVODKKYR 300
DB 241 VSDLOVSGLFFAIGHEPATKFLNGOLELHADGYVATKPGSTHTSVEGVFAAGDVODKKYR 300
QY 301 QAITAAGSCMAALDAHYLQEVGAQVGSZ 332
DB 301 QAITAAGSCMAALDAHYLQEVGAQVGSZ 332

RESULT 2

US-09-598-747-27
; Sequence 27, Application US/09598747
; Patent No. 6531648
; GENERAL INFORMATION:
; APPLICANT: Lananhan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gasdaska, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; TITLE OF INVENTION: THEREIN
; FILE REFERENCE: A-31383P1
; CURRENT APPLICATION NUMBER: US/09/598,747
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-598-747-27

Query Match 86.1%; Score 1469; DB 4; Length 310;
Best Local Similarity 91.6%; Pred. No. 1.5e-153;
Matches 283; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 1 MEGSAAAPTRVCIIGSGPAHTAAYAAAEKLVPEGWANDIAAGGQTTTTTVE 60
DB 1 MEGSAGAPLTRCIIGSGPSAHTAAYAAAEKLVPEGWANDIAAGGQTTTTTVE 60
QY 61 NFGPPTGIMDILMNCRAQSVRFGTNISETVTEVDFSAFPRVTSSTVLADTVV 120
DB 61 NFGPPEGLIGLMDRCRAQSRFGTSLISETVAVDFSAFPRVTSSTVLADTVV 120
QY 121 ATCAVARLHFGSDTYWNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEGNFLTKYG 180
DB 121 ATCAVARLHFGSDTYWNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEGNFLTKYG 180
QY 181 SQVYIHRNTFRASKIMOARALSNPKIOVWDSEVVEYAGGAGGGLAGVKVKNLVTGE 240
DB 181 SHVYIHRNTFRASKIMOARALSNPKIOVWDSEVVEYAGGAGGGLAGVKVKNLVTGE 240
QY 241 VSDLOVSGLFFAIGHEPATKFLNGOLELHADGYVATKPGSTHTSVEGVFAAGDVODKKYR 300
DB 241 ISDLQVSGLFFAIGHEPATKFLNGOLELHADGYVATKPGSTHTSVEGVFAAGDVODKKYR 300
QY 301 QAITAAGSG 309
DB 301 QAITAAGSG 309

RESULT 3

US-09-598-747-25
; Sequence 25, Application US/09598747
; Patent No. 6531648
; GENERAL INFORMATION:
; APPLICANT: Lananhan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gasdaska, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; TITLE OF INVENTION: THEREIN
; FILE REFERENCE: A-31383P1
; CURRENT APPLICATION NUMBER: US/09/598,747
; CURRENT FILING DATE: 2000-06-21

; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-598-747-25

Query Match 76.0%; Score 1296; DB 4; Length 333;
Best Local Similarity 76.6%; Pred. No. 2e-134;
Matches 249; Conservative 33; Mismatches 39; Indels 4; Gaps 1;

QY 11 TRVCIIGSGPAHTAAYAAAEKLVPEGWANDIAAGGQTTTTTVDENFGPFTGIM 70
DB 9 TRLCIVSGPAHTAAYAAAEKLVPEGWANDIAAGGQTTTTTVDENFGPFTGIM 68
QY 71 GIDLMNCRAQSVRFGTNISETVTEVDFSAFPRVTSSTVLADTVVATGAVARRLH 130
DB 69 GVELTDKFRKQSERFGTTTFTETVTVKVDFSSKPKLFTDSKAILADAVILAIGAVAKWLS 128
QY 131 FSGSDT---YMRGISACAVCDGAAPIFRNKPIAVIGGDSAMEGNFLTKYGSOVYII 186
DB 129 FVSGEVLGGLMNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEGNFLTKYGSOVYII 188
QY 187 HRRNTFRASKIMOARALSNPKIOVWDSEVVEYAGGAGGGLAGVKVKNLVTGEVSDQV 246
DB 189 DRDAPFRASKIMOARALSNPKIOVWNSVVEAYGDERDLGGLKYNVVTGDSVSLKV 248
QY 247 SGLFFAIGHEPATKFLNGOLELHADGYVATKPGSTHTSVEGVFAAGDVODKKYRQAITAA 306
DB 249 SGLFFAIGHEPATKFLNGOLELHADGYVATKPGSTHTSVEGVFAAGDVODKKYRQAITAA 308
QY 307 GSGCMAALDAHYLQEVGAQVGSZ 331
DB 309 GTGCMAALDAHYLQEVGAQVGSZ 333

RESULT 4

US-09-540-014-24
; Sequence 24, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Calliau, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; TITLE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-540-014-24

Query Match 73.3%; Score 1250.5; DB 4; Length 332;
Best Local Similarity 74.8%; Pred. No. 2.1e-129;
Matches 243; Conservative 33; Mismatches 44; Indels 5; Gaps 2;

QY 11 TRVCIIGSGPAHTAAYAAAEKLVPEGWANDIAAGGQTTTTTVDENFGPFTGIM 70

Db 9 TELCTVIGSGPAATTAATTAARAEKLPFLFEGWMANDIAAGGQLNQPPR-ENFPFPGPIL 67
QY 71 GIDLMNCRQAQSVRFGTNIISLSTVTEVDFSPARPRVTSDSTTVLADTVVATGAVARRLH 130
Db 68 GVELTDKFRKQSERFGTTFITETVTKVDFSSKPKLFTDSKAILADAVILAIGAVAKWLS 127
QY 131 FSGSDT---YNRGISACVCDGAAPFRNKPIAVIGGDSAMEEGNFKTKYGSQVYII 186
Db 128 FVGSSEVLGGLWNRGISACVCDGAAPFRNKPIAVIGGDSAMEEGNFKTKYGSQVYII 187
QY 187 HERNTRFRASKINQARALSNPKIQVWVDSEVVEAYGAGGGLAGVKKVNLVTGVSVDLQV 246
Db 188 DRDADFASKINQARALSNPKIDVWNSVVEAYGGERDVLGLKVKNNVTVGDVSDLVK 247
QY 247 SGLFPAIGHPATKFLNGOLELHAGDYATKPGSTHTSVGVPFAAGDVODKKYQAITAA 306
Db 248 SGLFPAIGHPATKFLDGGVELDSGYVVTGKTQTTSVPGVFAAGDVODKKYQAITAA 307
QY 307 GSGCMAALDAEHLQEVGAQVQKSD 331
Db 308 GTGCMALDAEHLQEVGAQVQKSD 332
RESULT 5
US-08-386-729A-7
; Sequence 7, Application US/08386729A
; Patent No. 5753435
; GENERAL INFORMATION:
; APPLICANT: Aharonowitz, Yair
; APPLICANT: Van Der Voort, Lucia H. M.
; APPLICANT: Cohen, Gerald
; APPLICANT: Bovenberg, Roelof A. L.
; APPLICANT: Schreiber, Rachel
; APPLICANT: Argaman, Anat
; APPLICANT: Av-Gay, Yossef
; APPLICANT: Nan, Helena M.
; APPLICANT: Kattewilder, Alfred
; APPLICANT: Pallissa, Harriet
; TITLE OF INVENTION: An oxido reductase enzyme system
; TITLE OF INVENTION: obtainable from P. chrysogenum, the set of genes
; TITLE OF INVENTION: encoding the same and the use of oxido reductase enzyme
; TITLE OF INVENTION: systems or genes encoding the same for increasing antibiotic
; TITLE OF INVENTION: production
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weill, Gotshal & Manges
; STREET: 2882 Sand Hill Road, Ste. 280
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/386,729A
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/274,043
; FILING DATE: 12-JULY-1994
; APPLICATION NUMBER: US 07/820,688
; FILING DATE: 24-MARCH-1992
; APPLICATION NUMBER: PCT/NL91/000101
; FILING DATE: 18-JUNE-1991
; APPLICATION NUMBER: EP 90201598.1
; FILING DATE: 18-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Venter, Barbara
; REGISTRATION NUMBER: 32,750

REFERENCE/DOCKET NUMBER: GBRO-024/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-386-729A-7
Query Match 55.6%; Score 948; DB 1; Length 334;
Best Local Similarity 56.2%; Pred. No. 5.2e-96;
Matches 181; Conservative 62; Mismatches 71; Indels 8; Gaps 2;
QY 9 LRTRVCIIGSGPAATTAATTAARAEKLPVLFEWMANDIAAGGQLTTTDDVENFPFGPTG 68
Db 2 VHSKVLIIGSGPAATTAATTAARAEKLPVLFEWMANDIAAGGQLTTTDDVENFPFGPTG 61
QY 69 IMGIDLMNCRQAQSVRFGTNIISLSTVTEVDFSPARPRVTSD-----STTVLADTVVVA 121
Db 62 IGGAEIADMNRAQSERFGTTEIITETISKLDSRPFKMWTWMDDEGSEPRVTADAVIA 121
QY 122 TGAVARRLHFSGSDTYWNRGISACVCDGAAPFRNKPIAVIGGDSAMEEGNFKTKYGS 181
Db 122 TGAVARRLNLPGSEETYWNGISACVCDGAAPFRNKPLVYIGGDSAAEAMFLAKYGS 181
QY 182 QVYTIHRRNTFRASKINQARALSNPKIQVWVDSEVVEAYG-GAGGGPLAGVKVNLVTGE 240
Db 182 SVTVLVRKDKLRASINIVADLLAHPKCKVRFTVATEVIGENKPNGLMTHLRVKDVLNA 241
QY 241 VSDIQVSLGFLPAIGHPATKFLNGOLELHAGDYATKPGSTHTSVGVPFAAGDVODKKYR 300
Db 242 EEVVEANGFLYAVGHDPASGLVRGQVELDDGYIITKPGTSFTNVEGVFACGDVODKKYR 301
QY 301 QAITAAGSGCMAALDAEHLQEV 322
Db 302 QAITAAGSGCMAALDAEHLQEV 323
RESULT 6
US-09-198-452A-331
; Sequence 331, Application US/09198452A
; Patent No. 5559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 331
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-331
Query Match 53.4%; Score 910.5; DB 4; Length 311;
Best Local Similarity 55.1%; Pred. No. 6.4e-92;
Matches 173; Conservative 61; Mismatches 73; Indels 7; Gaps 3;
QY 9 LRTRVCIIGSGPAATTAATTAARAEKLPVLFEWMANDIAAGGQLTTTDDVENFPFGPTG 68
Db 2 IHSRLIIGSGPSGYTAIVASRALHPLLEFEGFSG--ISGGQLMTTTEVENFPFGPEG 59
QY 69 IMGIDLMNCRQAQSVRFGTNIISLSTVTEVDFSPARPRVTSDSTTVLADTVVATGAVARR 128
Db 60 ILGPKLMNNKEQAVRFGTKTLAQDIISVDFSRPFLKSKETYSKDCIATGASAKR 119
QY 129 LHF--SGSDTYWNRGISACVCDGAAPFRNKPIAVIGGDSAMEEGNFKTKYGSQVYII 186

Db 120 LEIPGAGNDEFWQKGVTA CAVCDGASPIFNKDLYVIGGDSALLEALYLTRYGSHYVV 179
Qy 187 HRNRTFRASKIMQARALSNPKIQVWVDSVEVYECGAGGPGPACGKVKVNLVTGEVSDLOV 246
Db 180 HRDRLKASKAMEARQONNEKITPLWNSIYVKI--SGDSIVRSVDIKVQTOBITTREA 236
Qy 247 SGLPFAIGHPEPATKFLNGQLHLDADGYVATKPGSTHTSVGCVFAAGDVQDKYQRAITAA 306
Db 237 AGVFFAIGHKPTDFLGGOLTLDSEGYIVTERGTSKTSVPGVFAAGDVQDKYQRAVISA 236
Qy 307 GSGCMAALDAEHL 320
Db 297 GGGCIAALDAERFL 310

RESULT 7
US-09-328-352-5678
; Sequence 5678, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5678
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5678

Query Match 41.5%; Score 707.5; DB 4; Length 320;
Best Local Similarity 45.3%; Pred. No. 1.7e-69;
Matches 145; Conservative 57; Mismatches 101; Indels 17; Gaps 6;

Qy 11 TRVCIIGSGPAAHTAAIYAARAEKLPVLEPGWANDIAAGGQLTTTDDVENFPQPGTGM 70
Db 11 SRLIILGSGPAGYSAAYAAARANKPTLIAG----LQLGGQLTTTTEVDNWPDPGLT 65
Qy 71 GIDIMNCRQSVRGFTNLSETVDFPSAPRFTVSDSTTVLADTVVATGAVARLH 130
Db 66 GPALMDRMQHAERFTELYVDHINEVDLNVRFVLKGDMEYTCDAIILIATGATAQLG 125
Qy 131 FSGSDTYWNRGISACAVCDGAAPIFNKPIAVIGGDSAMEEGNLTKYGSQVYIHRN 190
Db 126 LSESEQFMGGVSACATCDGF--FYKNQNVWVGGGNTAVEEALYLSIAEHVTLVHRD 183
Qy 191 TPFRASKIMQARALSNP--KIQVWVDSVEVYECGAGGPGPACGKVKVNLVTGEVSDLOVS 247
Db 184 SLRSEKTLQHLFAKEKEGKISIVMNHVEEVJGNTG--VTGVRKSKTKDDSKQEVQV 241
Qy 248 GLRFAIGHPEPATKFLNGQLHLDADGYVATKPG----STHTSVGCVFAAGDVQDKYQRAI 303
Db 242 GLRFAIGHKPTDFLGGOLTLDSEGYIVTERGTSKTSVPGVFAAGDVQDKYQRAVISA 300
Qy 304 TAAGSGCMAALDAEHLQEV 323
Db 301 TSAGSGCMAALDAEKYLDNL 320

RESULT 8
US-09-328-352-8114
; Sequence 8114, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352


```

191  T'PRASKIMOARAL-----SNPKIOVVDSEVVEAYGGAGGGAGVGVKVNVLVTGE-VSDLOV 246
      :|||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
207  SPFAAEKILIKRLMDKVASGNIVLHTDRTLLEVTGDQMG--VSLRLRDTKNSDINVESLEV 264
      :|||::||::||::||::||::||::||::||::||::||::||::||::||::||
247  SGLFPAIGHPEATKFLNQLQLHLDGADGVATKPG-----STHTSVEGVFAAGDVQDKKYROA 302
      :|||::||::||::||::||::||::||::||::||::||::||::||::||::||
265  AGLFVAIGHSPNTAIFEQGLELE-NGYIKVQSGIHGNATQTSIPGVFAAGDVMDHIYROA 323
      :|||::||::||::||::||::||::||::||::||::||::||::||::||::||
303  ITAAGSGCMALDAEHYL 320
      :|||::||::||::||::||::||::||::||::||::||::||::||::||
324  ITSAGTGCNALDAERYL 341
      :|||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 10
US-09-543-681A-5633
; Sequence 5633, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEIN
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5633
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5633

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[illegible]

```

RESULT 11
US-09-252-991A-29849
; Sequence 29849, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

```

[illegible]

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RESULT 12
US-09-540-014-25
; Sequence 25, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillau, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; TITLE OF INVENTION: NADP-Thioedoxin Reductase
; FILE REFERENCE: 2001-070130
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 321
; TYPE: PR1
; ORGANISM: Escherichia coli
;
US-09-540-014-25

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Query Match 39.5%; Score 674; DB 4; Length 321;
Best Local Similarity 45.3%; Pred. No. 8.5e-66;

Query Match	31.8%;	Score	542.5;	DB	4;	Length	310;
Best Local Similarity	39.2%;	Pred.	No. 2.6e-51;				
Matches	122;	Conservative	57;	Mismatches	121;	Indels	11;
Gaps	5;						
Qy	13	VCIIIGSPAAHTAAYAAAEALKPVLFGWWMANDIAAGGQLTTTDDVENFPGPFTCI	MI	72			
		: : : : : : : : : : :					
Db	10	VIIIGAGPAGMTAAYAGKSNLSVLMIERG-----AFGQGMNTAEVENYPGFDS-IMGP	63				
		: : : : : : : : : : :					
Qy	73	DLMDNCRAQSVFGRNIISETVTVDFSGRPRFTSDSTVLADTVVAVTAVARRLHFS	132				
		: : : : : : : : : : :					
Db	64	ELAYKMYENVFEGTENAYGIVMGIEDHGSYKEVICDDKSYEAKAVIIATGCEHKLGVK	123				
		: : : : : : : : : : :					
Qy	133	GSPTYNWRGISACVCDGAAPIFRNKPIAVTIGGDSAMEBGNFLTXYGSOVYIIHRNTF	192				
		: : : : : : : : : : :					
Db	124	GESEFAGRGVSYCAVCDGA--FFKNKRLVWVGGDSSAVEAIVLTQPASEWVIVHRRDEL	181				
		: : : : : : : : : : :					
Qy	193	RASKTIQARALSNPKIQVTWDSSEVYEAAGGAGGFLAGVKVKNLVTGEVSDLQVSLFPA	252				
		: : : : : : : : : : :					
Db	182	RAQKIIQDRAPANEKISFVMDTVWEIYVGNTE--MVTGVKARNVKTDEVEIEANGVFYI	239				
		: : : : : : : : : : :					
Qy	253	IGHEPATKFLNGQLHDAHGVYATKPGSTHTSVSEGVPAAGVODKKYRQAITAAGSGCMA	312				
		: : : : : : : : : : :					
Db	240	VGLDPLTEPPFKAGITNEAGNIETDQ--EWRTYIPGVVAIGDVEKTLQITTAIVGEGGIA	298				
		: : : : : : : : : : :					
Qy	313	ALDAEHYLOEV	323				

US-09-598-747-7									
Query Match									
Best Local Similarity 34.2%; Pred. No. 9.2e-37;									
Matches 106; Conservative 48; Mismatches 139; Indels 17; Gaps 8;									
Qy	13	VCHIGGPA	AH	TA	IA	YAA	AE	LK	PV
Db	4	VAII	GGG	PAG	L	TA	AL	Y	S
Qy	73	DLMD	NC	RA	Q	S	V	R	F
Db	57	ELLE	K	M	K	E	Q	A	V
Qy	133	GSD	T	Y	M	R	G	I	S
Db	117	GES	A	F	I	G	R	V	S
Qy	193	R	A	S	K	I	M	A	R
Db	175	R	A	E	K	A	L	-	V
Qy	253	I	G	H	E	P	A	T	K
Db	231	I	G	M	E	P	A	T	D
Qy	311	M	A	L	D	A	E	H	L
Db	289	V	A	A	I	S	A	V	K

Search completed: June 21, 2004, 14:02:47
Job time : 23 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2004, 19:44:11 ; Search time 505 Seconds
(without alignments)
3011.726 Million cell updates/sec

Title: US-10-091-841A-9
Perfect score: 1706
Sequence: 1 MEGSAAPLTRVCIIGSP.....ALDAHYLQEVGAQVCKSDZ 332

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_epool/US10091841/runat_21062004_163838_28623/app_query.fasta_1.519
-DB=Published Applications NA -QFMT=fastap -PREFIX=rnpb -MINMATCH=0.1
-LOOPECL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10091841@cgn1_1.221 @runat_21062004_163838_28623
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG_SCORE=0 -WAIT -DSBLOCK=100
-LONGLOG -DSV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
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4: /cgn2_6/ptodata/1/pubpna/US05_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
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12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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ALIGNMENTS

RESULT 1
US-10-091-841-10
; Sequence 10, Application US/10091841
; Publication No. US20030150010A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioresdoxin and
; TITLE OF INVENTION: NADP-Thioresdoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/10/091,841
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/540,014
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21

1	1628	95.4	995	15	US-10-091-841-10	Sequence 10, Appl
2	1628	95.4	995	15	US-10-091-841-23	Sequence 23, Appl
3	1581	92.7	1286	13	US-10-425-114-5073	Sequence 5073, Ap
4	1581	92.7	1286	13	US-10-425-114-3716	Sequence 3716, Ap
5	1469	86.1	1560	15	US-10-306-292-26	Sequence 26, Appl
6	1346.5	78.9	1152	9	US-09-938-842A-2486	Sequence 2486, Ap
7	1346.5	78.9	1152	11	US-09-938-842A-2486	Sequence 2486, Ap
8	1324	77.6	1002	9	US-09-897-898-1	Sequence 1, Appl
9	1324	77.6	1002	9	US-09-897-898-2	Sequence 2, Appl
10	1324	77.6	1002	13	US-09-897-425-36	Sequence 36, Appl
11	1324	77.6	1002	13	US-09-897-425-37	Sequence 37, Appl
12	1324	77.6	1002	15	US-10-032-201B-8	Sequence 8, Appl
13	1324	77.6	1002	15	US-10-032-201B-10	Sequence 10, Appl
14	1324	77.6	1344	13	US-10-290-072-238	Sequence 238, App
15	1324	77.6	3787	9	US-09-897-898-13	Sequence 13, Appl
16	1324	77.6	3787	13	US-09-897-425-48	Sequence 48, Appl
17	1324	77.6	3787	15	US-10-032-201B-22	Sequence 22, Appl
18	1324	77.6	4545	9	US-09-897-898-18	Sequence 18, Appl
19	1324	77.6	4545	13	US-09-897-425-53	Sequence 53, Appl
20	1324	77.6	4545	15	US-10-032-201B-27	Sequence 27, Appl
21	1324	77.6	4546	9	US-09-897-898-15	Sequence 15, Appl
22	1324	77.6	4546	13	US-09-897-425-50	Sequence 50, Appl
23	1324	77.6	4546	15	US-10-032-201B-24	Sequence 24, Appl
24	1324	77.6	6357	13	US-10-290-072-38	Sequence 38, Appl
25	1324	77.6	6357	13	US-10-290-072-42	Sequence 42, Appl
26	1324	77.6	6357	15	US-10-141-531-38	Sequence 38, Appl
27	1324	77.6	6357	15	US-10-141-531-42	Sequence 42, Appl
28	1312	76.9	6357	13	US-10-290-072-35	Sequence 35, Appl
29	1312	76.9	6357	13	US-10-290-072-45	Sequence 45, Appl
30	1312	76.9	6357	15	US-10-141-531-35	Sequence 35, Appl
31	1312	76.9	6357	13	US-10-141-531-45	Sequence 45, Appl
32	1311	76.8	6357	13	US-10-290-072-37	Sequence 37, Appl
33	1311	76.8	6357	15	US-10-141-531-37	Sequence 37, Appl
34	1310	76.8	1345	13	US-10-290-072-215	Sequence 215, App
35	1310	76.8	6357	13	US-10-290-072-34	Sequence 34, Appl
36	1310	76.8	6357	13	US-10-290-072-40	Sequence 40, Appl
37	1310	76.8	6357	13	US-10-290-072-44	Sequence 44, Appl
38	1310	76.8	6357	15	US-10-141-531-34	Sequence 34, Appl
39	1310	76.8	6357	15	US-10-141-531-40	Sequence 40, Appl
40	1310	76.8	6357	13	US-10-141-531-44	Sequence 44, Appl
41	1309	76.7	6357	13	US-10-290-072-43	Sequence 43, Appl
42	1309	76.7	6357	13	US-10-290-072-46	Sequence 46, Appl
43	1309	76.7	6357	15	US-10-141-531-43	Sequence 43, Appl
44	1309	76.7	6357	15	US-10-141-531-46	Sequence 46, Appl
45	1308	76.7	6357	13	US-10-290-072-29	Sequence 29, Appl

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; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-10-091-841-10

Alignment Scores:
Pred. No.: 4,55e-196 Length: 995
Score: 1628.00 Matches: 328
Percent Similarity: 98.80% Conservative: 0
Best Local Similarity: 98.80% Mismatches: 3
Query Match: 95.43% Indels: 3
DB: 15 Gaps: 0

US-10-091-841A-9 (1-332) x US-10-091-841-10 (1-995)

QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgValCysIleIleGlySerGlyPro 20
DB 1 ATGGAGGGATCCGCGCGCGCGCTCCGACACGCGGTGTGCATCATCGGACGGCGCG 60
QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuYsProValLeuPheGlu 40
DB 61 GCGCGCACACGCGCGCGCTACGCGGCCGCGCGAGCTCAAGCCGCTCTTCGAG 120
QY 41 GlyTyrMetAlaAsnAspIleAlaAlaGlyGlnLeuThrThrThrThrThrThrThr 60
DB 121 GCGTGGATGGCCACGACATCCGCGCGGGGGCCAGCTCACCACACCGACGCTCGAG 180
QY 61 AsnPheProGlyPheProThrGlyIleMetGlyIleAspLeuMetAspAsnCysArgAla 80
DB 181 AACTTCCCGGATTCGCCACCGCATCGGCGCATCGGCGCATCGACCTCATGGACAAC 240
QY 81 GlnSerValArgPheGlyThrIleLeuSerGluThrValThrGluValAspPheSer 100
DB 241 CAGTCGTCGCTTCGCGACCAACATCTCTCCGAGACCGTCCGAGGTCGACTTCCTCC 300
QY 101 AlaArgProPheArgValThrSerAspSerThrThrValLeuAlaAspThrValVal 120
DB 301 GCGCGGCCCTTCGCGCTCACTCCGACTCCACACCGCTCCGCGGACACCGCTCGCTC 360
QY 121 AlaThrGlyAlaValAlaArgArgLeuHisPheSerGlySerAspThrTyrTrpAsnArg 140
DB 361 GCCACGGCGCGCTCCGCGCGCGCTCCATTTCTCCGGTTCGACACCTTACTGGAACCG 420
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnIysProIle 160
DB 421 GGCATCTCCGCTCGCGCTCTCGACGCGCGCTCGCGCCATCTTCGGGAACAAGCCCATC 480
QY 161 AlaValIleGlyGlyAspSerAlaMetGluGluGluAlaAsnPheLeuThrIysTyrGly 180
DB 481 GCGTTCATCGCGCGCGGTGATTCGCGCATGGAGGAAGCAACTTCCTCACCAGTACGGA 540
QY 181 SerGlnValTyrIleIleHisArgArgAsnThrPheArgAlaSerIysIleMetGlnAla 200
DB 541 TCCCAAGTGTACATATCCACGCGCGCAACACCTTCGCGCTCCCAAGATTATCGAGCT 600
QY 201 ArgAlaLeuSerAsnProIysIleGlnValValTrpAspSerGluValValGluAlaTyr 220
DB 601 AGGGCGCTCTCCATCTTAAGTCCAGGTTGTCTGGGACTC-GAGGTCTGTCGAGCTTAC 659
QY 221 GlyGlyValaGlyGlyProLeuAlaGlyValIysValIysAsnLeuValThrGlyGlu 240
DB 660 GCGCGTGCAGCGCGCGCCATAGCTGGGTCAAGTCAAGTCAAGTCTGGTGTGAG 719
QY 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrIys 260
DB 720 GTGCTGACCTTCAGGTGTCCGGGCTTTCTTCGCCATCGGCGCATGAGCGCGCCACCA 779
QY 261 PheLeuAsnGlyGlnLeuGluLeuHisAlaAspGlyTyrValAlaThrIysProGlySer 280
DB 780 TTTCTCAATGGGACGCTTGGCTCCGATGGGTATGTGGCCACCAAGCGGCTCT 839
QY 281 ThrHisThrSerValGluGlyValPheAlaAlaGlyAspValGlnAspIysIysTyrArg 300
DB 840 ACACATACCAGTGTGGAGGGGTC-TTTGCTGCTGGAGACGTGCAGGATAAGAAGTATCGT 898
QY 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu-AspAlaGluHisTyrIle 320
DB 899 CAGGCCATTACTGCTGCTGATCAGGTTGCAATGGCTGCTTTGGGACGCCGACATATCT 958
QY 320 uGlnGluValGlyAlaGlnValGlyLysSerAsp 331
DB 959 GCAGGAGGTGGTGCACAGTGGGCAAGTCTGAT 992

RESULT 2
; Sequence 23, Application US/10091841
; Publication No. US20030150010A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioresdoxin and
; TITLE OF INVENTION: NADP-Thioresdoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/10/091,841
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/540,014
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-10-091-841-23

Alignment Scores:
Pred. No.: 4,55e-196 Length: 995
Score: 1628.00 Matches: 328
Percent Similarity: 98.80% Conservative: 0
Best Local Similarity: 98.80% Mismatches: 3
Query Match: 95.43% Indels: 3
DB: 15 Gaps: 0

US-10-091-841A-9 (1-332) x US-10-091-841-23 (1-995)

QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgValCysIleIleGlySerGlyPro 20
DB 1 ATGGAGGGATCCGCGCGCGCGCTCCGACACGCGGTGTGCATCATCGGACGGCGCG 60
QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuYsProValLeuPheGlu 40
DB 61 GCGCGCACACGCGCGCGCTACGCGGCCGCGCGAGCTCAAGCCGCTCTTCGAG 120
QY 41 GlyTyrMetAlaAsnAspIleAlaAlaGlyGlnLeuThrThrThrThrThrThrThr 60
DB 121 GCGTGGATGGCCACGACATCCGCGCGGGGGCCAGCTCACCACACCGACGCTCGAG 180
QY 61 AsnPheProGlyPheProThrGlyIleMetGlyIleAspLeuMetAspAsnCysArgAla 80
DB 181 AACTTCCCGGATTCGCCACCGCATCGGCGCATCGGCGCATCGACCTCATGGACAAC 240
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Qy 81 GlnSerValArgPheGlyThrAsnIleLeuSerGluThrValThrGluValAspPheSer 100
Db 241 CAGTCGGTCGGCTTCGGCACCAATCTCTCCGAGACCGTCACCGAGGTGCATCTCTCC 300

Qy 101 AlaArgProPheArgValThrSerAspSerThrValLeuAlaAspThrValValVal 120
Db 301 GCCGCGCCCTTCGGCTCAGCTCCGACTCCACCAACCGTCTCGCCGACCGCTGCTGCTC 360

Qy 121 AlaThrGlyAlaValAlaArgAlaGlyLeuHisPheSerGlySerAspThrTyrTrpAsnArg 140
Db 361 GCCACGGGCGCGCTCGCGCGCGCTCCCAATTTCTCGGGTTCCGACACCTACTTGGAAACCGC 420

Qy 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProfile 160
Db 421 GGCATCTCCGCTCCGCGCTCTCGACGGCGCTCGGCCCATCTTCGCGAACAGGCCATC 480

Qy 161 AlaValIleGlyGlyAspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGly 180
Db 481 GCGGTCAATCGCGCGCGGTGATTCGCCCATCGAGGAAAGGCAACTTCCTCAACCAAGTACGGA 540

Qy 181 SerGlnValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db 541 TCCCAAGTGATACATCATCCAGCGCGCAACCTTCGCGCCCTCCAAAGATTATGCAAGCT 600

Qy 201 ArgAlaLeuSerAsnProLysIleGlnValValTrpAspSerGluValValGluAlaTyr 220
Db 601 AGGCGGCTCTCCAATCTCAAGATCCAGGTGTCTGGGACTC - GAGGTCTCGAGGCTTAC 659

Qy 221 GlyGlyAlaGlyGlyProLeuAlaGlyValLysValLysAsnLeuValThrGlyGlu 240
Db 660 GCGCGGTGACGCGCGCGCCCATTAGCTGGGCTCAAGGTCAAGAACTTGTGTGACTGTGTAG 719

Qy 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db 720 GTGTCTGACCTTCAGGTGTCTCGGCTTCTTCGCCATCGGATCGGACATGAGCGGCCACCAAG 779

Qy 261 PheLeuAsnGlyGlnLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGlySer 280
Db 780 TTCTCAATGGGACGCTTGAAGTCCATCGCGATGGGTATGTGGCCACCAAGCGCGGCTCT 839

Qy 281 ThrHisThrSerValGluGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg 300
Db 840 ACACATACCAAGTGTGAGGGGCTC - TTGTGCTGTGGAGACGTGACGATTAAGATATCT 998

Qy 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu - AspAlaGluHisTyrLe 320
Db 899 CAGGCCATTAATCTGCTGCTGATCAGGTTCATGGCTGCTTTGGAGCGCGGACCTATCT 958

Qy 320 uGlnGluValGlyAlaGlnValGlyLysSerAsp 331
Db 959 GCAGGAGGTGGTGACACAGGTGGGCAAGTCTGAT 992

RESULT 3
US-10-425-114-5073
; Sequence 5073, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5073
; LENGTH: 1286
; TYPE: DNA
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; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: 700447274_FLI

US-10-425-114-5073

Alignment Scores:

Pred. No.:	5,99e-190	Length:	1286
Score:	1581.00	Matches:	304
Percent Similarity:	95.17%	Conservative:	11
Best Local Similarity:	91.84%	Mismatches:	16
Query Match:	92.67%	Indels:	0
DB:	13	Gaps:	0

US-10-091-841A-9 (1-332) x US-10-425-114-5073 (1-1286)

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Qy 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgValCysIleIleGlySerGlyPro 20
Db 58 ATGAGGGATCCGCGCGCGCTCCGCTCCGACGGCGATCTGCATCATCGGAGCGGTC 117

Qy 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
Db 118 GCTGCGCACACGGCAGCCATCTACGCGCGCGCGCGAGCTCAAGCTGTGCTCTCGAG 177

Qy 41 GlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60
Db 178 GCTGGATGGCAACGACATCGCGCGGGCGGCGAGCTCACCAACACCGACGCTCGAG 237

Qy 61 AsnPheProGlyPheProThrGlyIleMetGlyIleAspLeuMetAspAsnCysArgAla 80
Db 238 AACTTCCGCGGCTTCCCAACGGCATCATGGCGCGCGACCTATGGACAACTGCGCGCG 297

Qy 81 GlnSerValArgPheGlyThrAsnIleLeuSerGluThrValThrGluValAspPheSer 100
Db 298 CAGTCTCCGCTTGGCACCACCATCTCTCCGAGACCGTCACCGCGCTGACCTTTTCG 357

Qy 101 AlaArgProPheArgValThrSerAspSerThrThrValLeuAlaAspThrValVal 120
Db 358 GCCTGCCATTCGAGATTAGTGACAGCTCCACACCGCTCTCCGCGGATCGCGTTATCGTT 417

Qy 121 AlaThrGlyAlaValAlaAlaArgAlaGlyHisPheSerGlySerAspThrTyrTrpAsnArg 140
Db 418 GCCACGGGAGCGCTCGCGCGCGCTCCACTTCCCGCGGTCGATGCATACTTGAACCGCG 477

Qy 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProfile 160
Db 478 GGCATCTCCGCTGTGCGCTCTGTGACGCTGCCCGCCCATCTCCGTAACACGCCATC 537

Qy 161 AlaValIleGlyGlyAspSerAlaMetGluGlyAsnPheLeuThrLysTyrGly 180
Db 538 GCCGTATAGCGCGCGGAGCTCCGCTATGGAGGAGTCCAATTTCTCCACCAAGTACGCG 597

Qy 181 SerGlnValTyrIleIleHisArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db 598 TCCACGCTTACATCATCCACCGCGCAATACCTTCCGTGCTTCCAGATCATGAGGCC 657

Qy 201 ArgAlaLeuSerAsnProLysIleGlnValValTrpAspSerGluValValGluAlaTyr 220
Db 658 AGGCGCTTGAAGACCCCAAAATTAAAGTCTCTCTGGGACTCGGAAGTTGTGAGGCCAT 717

Qy 221 GlyGlyAlaGlyGlyProLeuAlaGlyValLysValLysAsnLeuValThrGlyGlu 240
Db 718 GCGCGCGCAAAACGGCGCGCCATTTGGTGGCTAAAGGTTAAGAACCTACTTAATGGTGAG 777

Qy 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db 778 GTCTCGGATCTTCAAGTGTCTGGCTCTTCTTCGCCATCGGCGATGAGCGCGGACCAA 837

Qy 261 PheLeuAsnGlyGlnLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGlySer 280
Db 838 TTCTCGGCGGACAGCTTGAACCTCGATTTCAGATGTTATGTGGAACCAACAGCCAGTTCC 897

Qy 281 ThrHisThrSerValGluGlyValPheAlaAlaGlyAspValGlnAspLysTyrArg 300
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Db 898 ACTCACACAGTGTAAGGGTGTATTTGGCTGGCGACGTGCAGGACCAAGAGTACCGT 957
Qy 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeu 320
Db 958 CAGGCCATTACTGCGCTGGATCAGGGTGCATGGCTGCAATGGACGCTGAGCACTACCTG 1017
Qy 321 GlnGluValGlyAlaGlnValGlySerAsp 331
Db 1018 CAGGAGATCGGTGCACAGGAGGGAAGTCTGAT 1050
RESULT 4
US-10-425-114-3716
; Sequence 3716, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 3716
; LENGTH: 1325
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700336177_FLI
US-10-425-114-3716
Alignment Scores:
Pred. No.: 6,26e-190 Length: 1325
Score: 1581.00 Matches: 304
Percent Similarity: 95.17% Conservative: 11
Best Local Similarity: 91.84% Mismatches: 16
Query Match: 92.67% Indels: 0
DB: 13 Gaps: 0

US-10-091-841A-9 (1-332) x US-10-425-114-3716 (1-1325)

Qy 1 MetGluGlySerAlaAlaProLeuArgThrArgValCysIleIleGlySerGlyPro 20
Db 87 ATGAGGGATCCGCGCGCTCCGCTCCGACGGGCATCTGCATCATCGGGAGCGGTCC 146
Qy 21 AlaAlaHisThrAlaAlaIleThrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
Db 147 GCTGGCACAGGAGCCATACGCGCCCGCGGAGCTCAAGCTGTGCTTTCGAG 206
Qy 41 GlyTrpMetAlaAsnAspIleAlaAlaGlyGlnLeuThrThrThrThrAspValGlu 60
Db 207 GGTGGATGGCAACGACATCGCGCGCGCGGCGAGCTCACCACCAACCGACGTCGAG 266
Qy 61 AsnPheProGlyPheProThrGlyIleMetGlyIleAspLeuMetAspAsnCysAtcAla 80
Db 267 AACTTCCCGGCTTCCCAACAGGATCATGCGCGCGCGGACCTCATGGACAATGCGCGCG 326
Qy 81 GlnSerValArgPheGlyThrAsnIleLeuSerGluThrValThrGluValAspPheSer 100
Db 327 CAGTCCCTCGCTTTGGCAACCAATCTCTCCGAGACCGTCAACGCGCTGCACTTTTCG 386
Qy 101 AlaArgProPheArgValThrSerAspSerThrThrValLeuAlaAspThrValVal 120
Db 387 GCCTGCCCATTCGAGTGTAGTGCAGACTCCCAACCGGCTCCGCGGATGCGGTATCGTT 446
Qy 121 AlaThrGlyAlaValAlaArgLeuHisPheSerGlySerAspThrThrThrAsnArg 140
Db 447 GCCACGGGAGCGTGCAGCGGGCGCTCCACTTCCCGGGTCCGATGCATCTGGAACCGC 506

Qy 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
Db 507 GGCATCTCCGCTGTGGCGTCTGTGACGGTGCCGCCCATCTTCCTGTAACAAGCCCATC 566
Qy 161 AlaValIleGlyGlyGlyAspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGly 180
Db 567 CCGCTCATAGCGGGCGGCGACTCCGCTATGGAGGAGTCCAAATTTCTCCCAAGTACGGC 626
Qy 181 SerGlnValTyrIleIleHisArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db 627 TCCACGCTCTACATCATCCACGCGCAATACCTTCGTCGCTTCCAAAGATCATGACGCC 686
Qy 201 ArgAlaLeuSerAsnProLysIleGlnValValTyrAspSerGluValValGluAlaTyr 220
Db 687 AGGCGCTTGAGAACCCCAAAATTAAGTCTCTGGGACTCGGAAGTTGTGAGGCGCTAT 746
Qy 221 GlyGlyAlaGlyGlyGlyProLeuAlaGlyValLysValLysAsnLeuValThrGlyGlu 240
Db 747 GCGCGCGCAACGCGCGGCCCATTCGCTGGCGTAAGGTTAAGAACCTACTCAATGGTGA 806
Qy 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db 807 GTCTCGGATCTTCAGTGTCTGGCTCTCTTCGCCATCGGCGCATGAGCCGCGACCAA 866
Qy 261 PheLeuAsnGlyGlnLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGlySer 280
Db 867 TTCTCTGGGCGGACAGCTTGAACCTCGATTTCAGATGGTTATGTGGAAACCAAGCCAGGTTCC 926
Qy 281 ThrHisThrSerValGluGlyValPheAlaAlaGlyAspValGlnAspLysIleTyrArg 300
Db 927 ACTCACACAGTGTAAAGGGTGTATTTGCTGCTGGGACGTGCGAGCAAGAAAGTACCGT 986
Qy 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeu 320
Db 987 CAGGCCATTACTCGCGCTGGATCAGGTCGATGGCTGCTGATTTGGACGCTGAGCACTACCTG 1046
RESULT 5
US-10-306-292-26
; Sequence 26, Application US/10306292
; Publication No. US20030145347A1
; GENERAL INFORMATION:
; APPLICANT: Laranhan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gasdaska, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; TITLE OF INVENTION: THEREIN
; FILE REFERENCE: A-31383P1
; CURRENT APPLICATION NUMBER: US/10/306,292
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US/09/598,747
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-306-292-26

Alignment Scores:
Pred. No.: 1,24e-175 Length: 1560
Score: 1469.00 Matches: 283
Percent Similarity: 95.47% Conservative: 12
Best Local Similarity: 91.59% Mismatches: 14
Query Match: 86.11% Indels: 0
DB: 15 Gaps: 0

US-10-091-841A-9 (1-332) x US-10-306-292-26 (1-1560)

Qy 1 MetGluGlySerAlaAlaProLeuArgThrArgValCysIleIleGlySerGlyPro 20
Db 406 ATGAGGAGATCCGCGGGGCGCGCTCCGACGCGCTGTCATCATCGGAGCGGGCG 465
Qy 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
Db 466 TCGCGGACACGCGGGGAGTCTACGCGCGCGCGGAGGCTCAAGCCGCTCTTCGAG 525
Qy 41 GlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60
Db 526 GGTGGTGTGCGCAACGATCGCGCGGGGGCGGAGCTCACCCACCCAGCGTCGAG 585
Qy 61 AsnPheProGlyPheProThrGlyIleMetGlyIleAspLeuMetAspAsnCysArgAla 80
Db 586 AACTTCCGGGGTTCCCGAGGGATCTCGCGCGGAGTCTAGATCGTCCGCGGCC 645
Qy 81 GlnSerValArgPheGlyThrAsnIleLeuSerGlnThrValThrGluValAspPheSer 100
Db 646 CAGTCCCTCCGGTTCCGACACGATCATCTCCGAGACCGTCCCGCGCTCTCTCC 705
Qy 101 AlaArgProPheArgValThrSerAspSerThrThrValLeuAlaAspThrValVal 120
Db 706 GCCCGCCCTTCCCGCTGCGCTCCGATCCACACCGTGTGCGCGAGCGCGTCTGTC 765
Qy 121 AlaThrGlyAlaAlaAlaArgLeuHisPheSerGlySerAspThrThrTyrAsnArg 140
Db 766 GCCACCGCGCGCTCGCGCGGAGTCCACTTCGCGGCTCCGACGCTACTGGAACCGC 825
Qy 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
Db 826 GGCATCTCAGCTCGCGCTGCGAGCGGGCGCCGCCAATCTTCAGAAACAAACCCATC 885
Qy 161 AlaValIleGlyGlyGlyAspSerAlaMetGluGlyAsnPheLeuThrLysTyrGly 180
Db 886 CGCGTATCGCGCGCGGCGACTCCCGCATGAGGAGTCCAACTTCCTCACCAGTACGGC 945
Qy 181 SerGlnValTyrIleIleHisArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db 946 TCCCATGTGTATCATCATCCACCGCGCAACCTTCGCGCGCTCCAGATCATGACGGCC 1005
Qy 201 ArgAlaLeuSerAsnProLysIleGlnValValTyrAspSerGluValValGluAlaTyr 220
Db 1006 AGGGGTTGTCAACCCCAAGATCCAGTTTCTGGGACTCTGAGGTCTCGCGGCTCTAC 1065
Qy 221 GlyGlyAlaGlyGlyGlyProLeuAlaGlyValLysValLysAsnLeuValThrGlyGlu 240
Db 1066 GCGCGGAGGGTGGAGGTCCATTCGCTGCTCAAGGTGAAGACTTGGTTACTTGGGAAG 1125
Qy 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db 1126 ATCTCCGACCTTCAGGTGTCGGTCTCTTCCTCGCATCGGACATGAACCGCGACGAG 1185
Qy 261 PheLeuAsnGlyGlnLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGlySer 280
Db 1186 TTTTCGCGGGGAGCTTTCAGTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1245
Qy 281 ThrHisThrSerValGluGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg 300
Db 1246 AGCCACACAGTGTGAAGGGGTCTTTCGCTGCGGGATGTGCGAGACAGAGATTCGC 1305
Qy 301 GlnAlaIleThrAlaAlaGlySerGly 309
Db 1306 CAGGCTATTACTCGCGCTGGATCAGT 1332

RESULT 6
US-09-938-842A-2486
; Sequence 2486, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2486
; LENGTH: 1152
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-2486

Alignment Scores:
Pred. No.: 2,66e-160 Length: 1152
Score: 1346.50 Matches: 258
Percent Similarity: 88.13% Conservative: 39
Best Local Similarity: 76.56% Mismatches: 31
Query Match: 78.93% Indels: 9
DB: Gaps: 2
US-10-091-841A-9 (1-332) x US-09-938-842A-2486 (1-1152)
Qy 4 SerAlaAlaAlaProLeu-----ArgThrArgValCysIleIleGlySer 18
Db 139 TCGCGCGCGCGCGCTCGACATCGGAACTCACAACCCNAGTTTGCATCGTCGAGT 198
Qy 19 GlyProAlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeu 38
Db 199 GGACACGACGACACACACGCGCGGATCTATGATCGAGAGCGAGCTTAAAGCTCTCTC 258
Qy 39 PheGluGlyTyrMetAlaAsnAspIleAlaGlyGlyGlnLeuThrThrThrThrAsp 58
Db 259 TTCGAAGGATGATGCTTAACGATCGCTCCCGCGGTCAATTAACACACACCGAC 318
Qy 59 ValGluAsnPheProGlyPheProThrGlyIleMetGlyIleAspLeuMetAspAsnCys 78
Db 319 GTCGAAACTTCCCTGGGTTCCTCAAGGTATCTCGGTATTGATATCGTGAGAAATTC 378
Qy 79 ArgAlaGlnSerValArgPheGlyThrAsnIleLeuSerGluThrValThrGluValAsp 98
Db 379 AGAAACAAATCGAGAGATTTGGAATCGATCGTTCACGGAACACTGTTAACAAAGTTGAT 438
Qy 99 PheSerAlaArgProPheArgValThrSerAspSerThrThrValLeuAlaAspThrVal 118
Db 439 TTCTCATCGAAACCGTTTAAAGCTATTCTGATTCGAGAACTGTTCCTCGCTGATTCGTA 498
Qy 119 ValValAlaThrGlyAlaValAlaArgArgLeuHisPheSerGlySerAspThr----- 136
Db 499 ATCATTTCTACTGGAGCTGTGCTAAACGCTTAGCTTCCTGATTCCTCGTGAAGGTAAT 558
Qy 137 -----TyrTyrAsnArgGlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIle 154
Db 559 GGTGGTTTGGATCGTGTATCTCCGCTTGTGCTGTTTGGCGAGCGAGCTGCTCGATT 618
Qy 155 PheArgAsnLysProIleAlaValIleGlyGlyAspSerAlaMetGluGluGlyAsn 174
Db 619 TTTAGGAATAAGCCTCTCTGCTTATTGCTGTGTGATTCAGCTATGGAGGAAGCGAAT 678
Qy 175 PheLeuThrLysTyrGlySerGlnValTyrIleIleHisArgAsnThrPheArgAla 194
Db 679 TTTCTGACTAAGTATGATCTAGGTTTATATTATTCATAGGAGGATACGTTTAGGGCG 738
Qy 195 SerLysIleMetGlnAlaArgAlaLeuSerAsnProLysIleGlnValValTyrAspSer 214
Db 739 TCTAAGATTATGACGACGAGAGCTTGTCTCAACCCCTAAGATTGAAGTATTGGAACCTC 798
Qy 215 GluValValGluAlaTyrGlyGlyAlaGlyGlyGlyProLeuAlaGlyValLysValLys 234

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Db      799  GCCGTGGTTAGGGCTATGGTATGAAATGGAGCTGTTCTTGGAGAGTTGAAGTGAAG 858
Qy      235  AsnLeuValThrGlyValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGly 254
Db      859  AATGTTGTTACTGGGGATGTTTCAGATCTGAAGGTGTCGATTTGTTCTTTGCTATTGGT 918
Qy      255  HisGluProAlaThrLysPheLeuAsnGlyGlnLeuGluLeuHisAlaAspGlyTyrVal 274
Db      919  CATGAGCCAGCTACCAAGATTTTGTATGGCAGCTTGAGCTTGATGAAGATGGTTATGTT 978
Qy      275  AlaThrLysProGlySerThrHisThrSerValGluGlyValPheAlaAlaGlyAspVal 294
Db      979  GTGACCAAGCCAGGTACTACTAAGACGAGCGTGGTTGGTATTTGCTGCGAGATGTT 1038
Qy      295  GlnAspLysLysTyrArgGlnAlaIleThrAlaIleThrAlaIleGlySerGlyCysMetAlaLeu 314
Db      1039  CAAGACAAGAGATAGACAGGCCCATCTCTGCGAGAACTGGGTGATGCGCGCATG 1098
Qy      315  AspAlaGluHisTyrLeuGlnGluValGlyAlaGlnValGlyLysSerAsp 331
Db      1099  GATGCAGAGCATTACTTACAAGAGATTGGATCTCAGGAGGGTAAGAGTGTAT 1149

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RESULT 7

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US-09-938-842A-2486
; Sequence 2486, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kregs, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2486
; LENGTH: 1152
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2486

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Alignment Scores:
Pred. No.:      2,668-160      Length:      1152
Score:          1346.50      Matches:    258
Percent Similarity: 88.13%      Conservative: 39
Best Local Similarity: 76.56%      Mismatches: 31
Query Match:     78.93%      Indels:     9
DB:              11          Gaps:        2

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US-10-091-841A-9 (1-332) x US-09-938-842A-2486 (1-1152)

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Qy      4  SerAlaAlaProLeu-----ArgThrArgValCysIleIleGlySer 18
Db      139  TCGCGCCGCGCGCGTGCAGATGGAACCTCAAAACCAAGTTTGCATCGTGGAAAT 198
Qy      19  GlyProAlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeu 38
Db      199  GGACCCAGCAGCACACACGCGCGGATCTATGATCGAGCGGAGCTTAAGCTTCTC 258
Qy      39  PheGluGlyTyrMetAlaAsnAspIleAlaAlaGlyGlnLeuThrThrThrAsp 58
Db      259  TTGGAAGGATGATGATGCTAACGACATCGCTCCGCGGCTCAATTAACACACACG 318
Qy      59  ValGluAsnPheProGlyPheProThrGlyIleMetGlyIleAspLeuMetAspAsnCys 78

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Db      319  GTCGAAACCTTCCCTGGGTTCCTGAAGGTATCTCGTATGATATCGTTGAGAAATTC 378
Qy      79  ArgAlaGlnSerValArgPheGlyThrAsnIleLeuSerGluThrValThrGluValAsp 98
Db      379  AGAAACCAATCGAGAGATTTGGAACTACGATCTTCACGGAACACTGTTAAACAAGTTGAT 438
Qy      99  PheSerAlaAspGlyProPheArgValThrSerAspSerThrThrValLeuAlaAspThrVal 118
Db      439  TTCTCATCGAAACCTTTAAGCTATTCAGTATTCAGAACTGTTCTCGCTGATTTCTGTA 498
Qy      119  ValValAlaThrGlyAlaValAlaAlaArgArgLeuHisPheSerGlySerAspThr----- 136
Db      499  ATCAATTCCTACTGAGAGCTGTTCTCTAAAGCTCTTAGCTTCTACTGGATCTGGTGAAGTAAT 558
Qy      137  -----TyrTrpAsnArgGlyLysSerAlaCysAlaValCysAspGlyAlaAlaProIle 154
Db      559  GGTGGTTTTTGGAACTCGTGATCTCCGCTTGTGCTGTTTGGACGAGAGCTGCTCGATT 618
Qy      155  PheArgAsnLysProIleAlaValIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 174
Db      619  TTAGGAATAAGCCTCTCTGCTGTTATTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 678
Qy      175  PheLeuThrLysTyrGlySerGlnValTyrIleIleHisArgArgAsnThrPheArgAla 194
Db      679  TTCTGACTAAGTATGATGATCTAAGGTTTATATATTATCATAGGAGGATACGTTTAGGGCG 738
Qy      195  SerLysIleMetGlnAlaAlaArgAlaLeuSerAsnProLysIleGlnValValTrpAspSer 214
Db      739  TCTAAGATTATGCAGCAGAGAGCTTTGTCTAACCCCTAAGATTGAAGTGAATTTGAACCTCT 798
Qy      215  GluValValGluAlaTyrGlyGlyAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 234
Db      799  GCGTGGTTGAGCGGTATGGTGAATGAAATGAGCGGTCTTCTGGAGGATGAAGGTGAAG 858
Qy      235  AsnLeuValThrGlyGluValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGly 254
Db      859  AATGTTGTTACTGGGATGTTTCAGATCTGAAGTCTGCGATTGTTCTTCTGCTATTGTT 918
Qy      255  HisGluProAlaThrLysPheLeuAsnGlyGlnLeuGluLeuHisAlaAspGlyTyrVal 274
Db      919  CATGAGCCAGCTACGAAGTTTTTGGATGGCGAGCTTGAGCTTGATGAAGATGGTTATGTT 978
Qy      275  AlaThrLysProGlySerThrHisThrSerValGluGlyValPheAlaAlaGlyAspVal 294
Db      979  GTGACCAAGCCAGGTACTACTAAGACGAGCGTGGTTGGTATTTGCTGCTGAGATGTT 1038
Qy      295  GlnAspLysLysTyrArgGlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu 314
Db      1039  CAAGACAAGAGATAGACAGGCCCATCTCTGCTGCGAGAACTGGGTGATGCGCGCATG 1098
Qy      315  AspAlaGluHisTyrLeuGlnGluValGlyAlaGlnValGlyLysSerAsp 331
Db      1099  GATGCAGAGCATTACTTACAAGAGATTGGATCTCAGGAGGGTAAGAGTGTAT 1149

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RESULT 8

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US-09-897-898-1
; Sequence 1, Application US/09897898
; Patent No. US20020037303A1
; GENERAL INFORMATION:
; APPLICANT: DECKERS, HARM M.
; APPLICANT: VAN ROOIJEN, GIJS
; APPLICANT: BOOTHIE, JOSEPH
; APPLICANT: GOLL, JANIS
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMIA, BIPIN K.
; TITLE OF INVENTION: THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
; TITLE OF INVENTION: BODY BASED PRODUCTS
; FILE REFERENCE: 034547/0104
; CURRENT APPLICATION NUMBER: US/09/897,898
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 09/577,147
; PRIOR FILING DATE: 2000-05-24

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;; PRIOR APPLICATION NUMBER: 09/448,600
;; PRIOR FILING DATE: 1999-11-24
;; PRIOR APPLICATION NUMBER: 09/084,777
;; PRIOR FILING DATE: 1998-05-27
;; PRIOR APPLICATION NUMBER: 60/047,753
;; PRIOR FILING DATE: 1997-05-27
;; PRIOR APPLICATION NUMBER: 60/047,779
;; PRIOR FILING DATE: 1997-05-28
;; PRIOR APPLICATION NUMBER: 60/075,863
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/075,864
;; PRIOR FILING DATE: 1998-02-25
;; NUMBER OF SEQ ID NOS: 24
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1
;; LENGTH: 1002
;; TYPE: DNA
;; ORGANISM: Unknown Organism
;; FEATURE:
;; LOCATION: (1)..(999)
;; NAME/KEY: CDS
;; OTHER INFORMATION: Description of Unknown Organism: Published NADPH
;; OTHER INFORMATION: thioredoxin reductase
US-09-897-898-1

Alignment Scores:
Pred. No.: 1.54e-157 Length: 1002
Score: 1324.00 Matches: 252
Percent Similarity: 88.00% Conservative: 34
Best Local Similarity: 77.54% Mismatches: 35
Query Match: 77.61% Indels: 4
DB: 9 Gaps: 1

US-10-091-841A-9 (1-332) x US-09-897-898-1 (1-1002)

Qy 11 ThrArgValCysIleLeuGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
Db 25 ACAAGGCTCTGTATCGTAGGAGTGGCCCGGACACACACGCGCGGATTACGGAGCT 84
Qy 31 ArgAlaGluLeuTyrProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaGly 50
Db 85 AGGGCTGAACCTTAAACCTCTCTTCGAAGGATGGCTAACGACATCGCTCCCGT 144
Qy 51 GlyGlnLeuThrThrThrThrAspValGluAsnPheProGlyPheProThrGlyIleMet 70
Db 145 GGTCAACTAAACACCCACCGAGCTGAGAAATTCCTCCCGGATTCACAGAGGTATTC 204
Qy 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
Db 205 GGAGTAGAGCTCACTGACAAATTCGTAACATCGGAGCGATTCGTACTACGATATT 264
Qy 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
Db 265 ACAGAGACGGTGACGAAGTCGATTTCTCTCGAAACCGTTTAAGCTATTACAGATTCA 324
Qy 111 ThrThrValLeuAlaAspThrValValAlaThrGlyValAlaAlaArgArgLeuHis 130
Db 325 AAAGCCATTCTCGTAGCGTGTGATTCGCTACTGGAGCTGTGGCTAAGCGGCTTAGC 384
Qy 131 Phe-----SerGlySerAspThrTyrTrpAsnArgGlyIleSerAlaCysAla 146
Db 385 TTCGTTGGATCTGGTGAAGGTTCTGGAGGTTCTCGAACCCTGGAACTCCGCTTCGCT 444
Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
Db 445 GTTTCGACGAGCTGCTCGATATTCGTAACAACTCTTCGGGTGATCGGTGGAGGC 504
Qy 167 AspSerAlaMetGluGluGlyAsnPheLeuThrIleTyrGlySerGlnValTyrIleIle 186
Db 505 GATTACCAATGGAAGAAGCAAACTTTCTTACAAATATGGAATCTAAAGGTATATAATC 564
Qy 187 HisArgArgAsnThrPheArgAlaSerIleLeuMetGlnAlaArgAlaLeuSerAsnPro 206

Db 565 CATAGGAGAGATGCTTTTAGAGCGCTTAAGATTATGACGAGCGAGCTTTCTTAATCCT 624
Qy 207 LysIleGlnValValTrpAspSerGluValValGluAlaIleTyrGlyAlaGlyGly 226
Db 625 AAGATTGATGTGATTGGAACTCTGTTGTGGAAGCTTATGAGATGGAGAAAGAGAT 684
Qy 227 ProLeuAlaGlyValValLysAsnLeuValThrGlyGluValSerAspLeuGlnVal 246
Db 685 GTGCTTGGAGGATTGAAGTGAAGAAATGTGGTTACCGAGAGATTTCTGATTTAAAGTT 744
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeu 266
Db 745 TCTGGATTGTTCTTTGCTATTGTCATGACGACGACTACCAAGTTTGGATGGTGGTGT 804
Qy 267 GluLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerValGlu 286
Db 805 GAGTTAGATTTCGGATGGTTATGTTGTCCAGAAAGCTGTGATCAGACACTAGCGTTCCC 864
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
Db 865 GGAGTTTTCGCTCGCGGTGATGTTTCAGGATAAAGATATATGGCAAGCCATCACTGCTGA 924
Qy 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluValGlyAlaGln 326
Db 925 GGAACCTGGGTGCATGGCAGCTTTGGATGCGACAGCATTAATTACAGAGATTTGGATCTCAG 984
Qy 327 ValGlyLysSerAsp 331
Db 985 CAAGTAAGATGAT 999

RESULT 9
US-09-897-898-2
; Sequence 2, Application US/09897898
; Patent No. US20020037303A1
; GENERAL INFORMATION:
; APPLICANT: DECKERS, HARM M.
; APPLICANT: VAN ROOIJEN, GIJS
; APPLICANT: BOOTHE, JOSEPH
; APPLICANT: GOLL, JANIS
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMIA, BIPIN K.
; TITLE OF INVENTION: THIOREDIXIN AND THIOREDIXIN REDUCTASE CONTAINING OIL
; TITLE OF INVENTION: BODY BASED PRODUCTS
; FILE REFERENCE: 034547/0104
; CURRENT APPLICATION NUMBER: US/09/897,898
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 09/577,147
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 09/448,600
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 09/084,777
; PRIOR FILING DATE: 1998-05-27
; PRIOR APPLICATION NUMBER: 60/047,753
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: 60/047,779
; PRIOR FILING DATE: 1997-05-28
; PRIOR APPLICATION NUMBER: 60/075,863
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/075,864
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(999)
US-09-897-898-2

Alignment Scores: 1.54e-157 Length: 1002
Pred. No.: 1002

```

Scores: 1324.00 Matches: 252
Percent Similarity: 88.00% Conservative: 34
Best Local Similarity: 77.54% Mismatches: 35
Query Match: 77.61% Indels: 4
DB: 9 Gaps: 1

US-10-091-841A-9 (1-332) x US-09-897-898-2 (1-1002)

QY 11 ThrArgValCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
DB 25 ACAAGGCTCTGTATCGTAGGAAGTGGCCGACACACACGGCGGCGATTTACGAGCT 84
QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaGly 50
DB 85 AGGCGTGAACCTTAAACCTCTTCTTCGAGGATGGATGCTTAACGACATCGCTCCCGGT 144
QY 51 GlyGlnLeuThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 70
DB 145 GGTCAACTAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 204
QY 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
DB 205 GGAGTAGAGCTCACTGACAAATTCGTAACATCGGAGCGATTCGGTACTACGATATT 264
QY 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
DB 265 ACAGAGACGGTGACAAAGTGGATTTCTCTCGAAACCGTTTAAGCTATTACAGATTCA 324
QY 111 ThrThrValLeuAlaAspThrValValAlaAlaThrGlyValAlaAlaArgArgLeuHis 130
DB 325 AAAGCCATTCTCGTACGCTGTGATTTCTCGTACTGGAGCTGGCTAAGCGGCTTAGC 384
QY 131 Phe-----SerGlySerAspThrTrpAsnArgGlyIleSerAlaCysAla 146
DB 385 TTGCTGGATCTGCTGAAGTCTCGAGGTTCTCGAACCCTCGAATCTCGCTTGCT 444
QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
DB 445 GTTTGCGACGAGCTGCTCGCATATTCGTAACAAACCTCTCGCGGTGATCGGTGGAGGC 504
QY 167 AspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGlySerGlnValTyrIle 186
DB 505 GATTCAGCAATGGAAGAAGCAAACTTCTTACAAAATATGGAATCTAAGATGTATATAATC 564
QY 187 HisArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuSerAsnPro 206
DB 565 CATAGGAGAGATGCTTTTAGAGCGCTCTAAGATTATGACGACGAGCTTTGTCTAATCCT 624
QY 207 LysIleGlnValValTrpAspSerGluValValGluAlaTyrGlyGlyAlaGlyGly 226
DB 625 AAGATTGATGTGATTGGAACCTCTGTTGTGGAAGCTTATGGAGATGAGAAAGAGAT 684
QY 227 ProLeuAlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGlnVal 246
DB 685 GTGCTTGAGAGATTGAAAGTGAAGAATGTGGTTACCGGAGATGTTTCTGATTTAAAGTT 744
QY 247 SerGlyLeuPheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeu 266
DB 745 TCTGATTGTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 804
QY 267 GluLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerValGlu 286
DB 805 GAGTTAGATTCCGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 864
QY 287 GlyValPheAlaAlaGlyAspValGlnAspLysValThrArgGlnAlaIleThrAlaAla 306
DB 865 CGAGTTTTCGCTGCGGTGATGTTCCAGTAAAGATATAGCCAGCCATCATCTGCTGCA 924
QY 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnValGlyAlaGln 326
DB 925 GGAACCTGGGTGCATGGCAGCTTTGGATGTCAGAGCATTACTTACAAGAGATTGGATCTCAG 984
QY 327 ValGlyLysSerAsp 331

Db 985 CAAGGTAAGAGTGAT 999

RESULT 10
US-09-897-425-36
; Sequence 36, Application US/09897425
; Publication No. US20020088025A1
; GENERAL INFORMATION:
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMIA, BIPIN K.
; TITLE OF INVENTION: PREPARATION OF THIOREDOXIN AND THIOREDOXIN REDUCTASE
; TITLE OF INVENTION: PROTEINS ON OIL BODIES
; FILE REFERENCE: 034547/0106
; CURRENT APPLICATION NUMBER: US/09/897,425
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/210,843
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/846,021
; PRIOR FILING DATE: 1997-04-25
; PRIOR APPLICATION NUMBER: 08/366,783
; PRIOR FILING DATE: 1994-12-30
; PRIOR APPLICATION NUMBER: 08/142,418
; PRIOR FILING DATE: 1993-11-16
; PRIOR APPLICATION NUMBER: 07/659,835
; PRIOR FILING DATE: 1991-02-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Published NADPH
; OTHER INFORMATION: thioredoxin reductase sequence
; NAME/KEY: CDS
; LOCATION: (1) .. (999)
US-09-897-425-36

Alignment Scores:
Pred. No.: 154e-157 Length: 1002
Score: 1324.00 Matches: 252
Percent Similarity: 88.00% Conservative: 34
Best Local Similarity: 77.54% Mismatches: 35
Query Match: 77.61% Indels: 4
DB: 13 Gaps: 1

US-10-091-841A-9 (1-332) x US-09-897-425-36 (1-1002)

QY 11 ThrArgValCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
DB 25 ACAAGGCTCTGTATCGTAGGAAGTGGCCGACACACACGGCGGCGATTTACGAGCT 84
QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaGly 50
DB 85 AGGCGTGAACCTTAAACCTCTTCTTCGAGGATGGATGCTTAACGACATCGCTCCCGGT 144
QY 51 GlyGlnLeuThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 70
DB 145 GGTCAACTAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 204
QY 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
DB 205 GGAGTAGAGCTCACTGACAAATTCGTAACATCGGAGCGATTCGGTACTACGATATT 264
QY 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
DB 265 ACAGAGACGGTGACAAAGTGGATTTCTCTCGAAACCGTTTAAGCTATTACAGATTCA 324
QY 111 ThrThrValLeuAlaAspThrValValAlaAlaThrGlyValAlaAlaArgArgLeuHis 130
DB 325 AAAGCCATTCTCGTACGCTGTGATTTCTCGTACTGGAGCTGGCTAAGCGGCTTAGC 384
QY 131 Phe-----SerGlySerAspThrTrpAsnArgGlyIleSerAlaCysAla 146
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Db 385 TTCTGTTGGATCTGGTGAAGTTCTCGAGGTTCTTCGGAACCGTGGAAATCTCCGCTGTGCT 444
Qy 147 ValCysAspGlyValAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
Db 445 GTTTCGCGAGGAGCTGCTCCGATATCCGATACAAACCTCTTCGGTGTATCGGTGAGGC 504
Qy 167 AspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGlySerGluValTyrIleIle 186
Db 505 GATTTCAGCAATGGAAGAGCAACCTTCTTACAAATATGATCTAAAGTGTATATATC 564
Qy 187 HisArgGAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuSerAsnPro 206
Db 565 CATAGAGAGATGCTTTTAGACGCTTAAGATATATGACGACGAGCTTTTGTCTAATCCT 624
Qy 207 LysIleGlnValValTyrAspSerGluValValGluAlaTyrGlyValAlaGlyGly 226
Db 625 AGATTGATGCTGATTGGAACTCGTCTGTGTGGAGCTTATGGAGATGGAGAAAGAT 684
Qy 227 ProLeuAlaGlyValLysValLysLeuValThrGlyGluValSerAspLeuGlnVal 246
Db 685 GTGCTTGGAGGATGAAAGTGAAGATGTGTTACCGGAGATGTTCTGATTTAAAGTT 744
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeu 266
Db 745 TCTGATGTTCTTGTCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 804
Qy 267 GluLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerValGlu 286
Db 805 GAGTTAGATTCTGATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 864
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
Db 865 GGAGTTTTCGCTGCGGCTGATGCTCAGGATAAGAGTATAGCAAGCCATCACTGCTGCA 924
Qy 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluValGlyAlaGln 326
Db 925 GGAACCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 984
Qy 327 ValGlyLysSerAsp 331
Db 985 CAAGGTAAGAGTGTAT 999

RESULT 11

US-09-897-425-37
; Sequence 37, Application US/09897425
; Publication No. US20020088025A1
; GENERAL INFORMATION:
; APPLICANT: MOLONEY, MAURICE M.
; TITLE OF INVENTION: PREPARATION OF THIOREDUXIN AND THIOREDUXIN REDUCTASE
; FILE REFERENCE: 034547/0105
; CURRENT APPLICATION NUMBER: US/09/897,425
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/210,843
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/846,021
; PRIOR FILING DATE: 1997-04-25
; PRIOR APPLICATION NUMBER: 08/366,783
; PRIOR FILING DATE: 1994-12-30
; PRIOR APPLICATION NUMBER: 08/142,418
; PRIOR FILING DATE: 1993-11-16
; PRIOR APPLICATION NUMBER: 07/659,835
; PRIOR FILING DATE: 1991-02-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS

; LOCATION: (1)..(999)
US-09-897-425-37

Alignment Scores:

Pred. No.: 1.54e-157 Length: 1002
Score: 1324.00 Matches: 252
Percent Similarity: 88.00% Conservative: 34
Best Local Similarity: 77.54% Mismatches: 35
Query Match: 77.61% Indels: 4
DB: 13 Gaps: 1

US-10-091-841a-9 (1-332) x US-09-897-425-37 (1-1002)

Qy 11 ThrArgValCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
Db 25 ACAAGGCTCTGTATCGTAGGAAGTGGCCACGAGCGCACACACGCGCGGATTTACGAGCT 84
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50
Db 85 AGGCGTGAACCTTAAACCTCTTCTTCGAAGGATGATGGCTAACGACATCGCTCCCGGT 144
Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProThrGlyIleMet 70
Db 145 GGTCAACTAACACACCCAGCGTGGAGATTTCCCGGATTTCCAGAGGATTTCTC 204
Qy 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
Db 205 GGAGTAGAGCTCACTGACAAATTCGTAACCAATCGGAGCGATTCGCTACTACGATATTT 264
Qy 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
Db 265 ACAGAGAGCGGTGACGAAGTCGATTTCTTTCGAACCGTTTAAGCTATTCACAGATTC 324
Qy 111 ThrThrValLeuAlaAspThrValValAlaAlaThrGlyAlaValAlaArgLeuHis 130
Db 325 AAAGCCATTCTCGCTACGCTGTGATTTCTCGCTACTGAGCTGTGGCTAAGCGCTTAGC 384
Qy 131 Phe-----SerglySerAspThrTyrTyrAsnArgGlyIleSerAlaCysAla 146
Db 385 TTCTGTTGGATCTGGTGAAGTTCTCGAGGTTCTGGAAACCGTGAATCTCCGCTTGTGCT 444
Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
Db 445 GTTTCGCGAGGAGCTGCTCCGATATTCGTAACAAACCTTCTCGGTGATCGGTGAGGC 504
Qy 167 AspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGlySerGlnValTyrIleIle 186
Db 505 GATTTCAGCAATGGAAGAGCAACCTTCTTACAAATATGATCTAAAGTGTATATATC 564
Qy 187 HisArgGAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuSerAsnPro 206
Db 565 CATAGGAGATGCTTTTAGAGCGTCTAAGATATATGACGACGAGCTTTTGTCTAATCCT 624
Qy 207 LysIleGlnValValTyrAspSerGluValValGluAlaTyrGlyAlaGlyGly 226
Db 625 AAGATTGATGATTTGGAACTCGTCTGTGTGGAGCTTATGGAGATGGAGAAAGAT 684
Qy 227 ProLeuAlaGlyValLysValLysLeuValThrGlyGluValSerAspLeuGlnVal 246
Db 685 GTGCTTGGAGGATGAAAGTGAAGATGTGTTACCGGAGATGTTCTGATTTAAAGTT 744
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeu 266
Db 745 TCTGATGTTCTTGTCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 804
Qy 267 GluLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerValGlu 286
Db 805 GAGTTAGATTCTGATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 864
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
Db 865 GGAGTTTTCGCTGCGGCTGATGCTCAGGATAAGAGTATAGCAAGCCATCACTGCTGCA 924

QY 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisThrLeuGlnGluValGlyAlaGln 326
 Db 925 GGAAGCTGGTGCATGGCAGCTTTGGATGCGAGCATTACTTACAGAGATTGGATCTCAG 984
 QY 327 ValGlyLysSerAsp 331
 Db 985 CAAGGTAAGAGTGAT 999

RESULT 12

US-10-032-201B-8
 ; Sequence 8, Application US/10032201B
 ; Publication No. US20030167524A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Rooijen, Gijls
 ; APPLICANT: Deckers, Harm
 ; APPLICANT: Heifetz, Peter Bernard
 ; APPLICANT: Briggs, Steven
 ; APPLICANT: Dalmia, Bipin Kumar
 ; APPLICANT: Del Val, Greg
 ; APPLICANT: Zaplachinski, Steve
 ; APPLICANT: Moloney, Maurice
 ; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
 ; FILE REFERENCE: 38814 351B
 ; CURRENT APPLICATION NUMBER: US/10/032,201B
 ; CURRENT FILING DATE: 2001-12-19
 ; NUMBER OF SEQ ID NOS: 313
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 1002
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana

US-10-032-201B-8 (1-332) x US-10-032-201B-8 (1-1002)

Alignment Scores:
 Pred. No.: 1.54e-157 Length: 1002
 Score: 1324.00 Matches: 252
 Percent Similarity: 88.00% Conservative: 34
 Best Local Similarity: 77.54% Mismatches: 35
 Query Match: 77.61% Indels: 4
 DB: 15 Gaps: 1

US-10-091-841A-9 (1-332) x US-10-032-201B-8 (1-1002)
 QY 11 ThrArgValCysIleleGlySerGlyProAlaAlaHisThrAlaAlaIleThrAlaAla 30
 Db 25 ACAAGGCTCTGTATCGTAGGAATGGCCCGCCGACACACGCGCGGATTTACGCGAGCT 84
 QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 50
 Db 85 AGGCTGAACCTTAACTCTCTCTTCGAAGGATGATGGCTAACGACATCGCTCCCGT 144
 QY 51 GlyGluLeuThrThrThrAspValGluAsnPheProGlyPheProThrGlyIleMet 70
 Db 145 GGTCAACTAACACACACACCGCGCGTGGAGATTTCCCGCGGATTTCCAGAGGATTTCTC 204
 QY 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
 Db 205 CGAGTAGAGCTCACTGACAAATTCCTTAACATCGAGCGATTGGTACTACGATATT 264
 QY 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
 Db 265 ACAGACCGGTGACGAAGTCGATTTCTCTCGAAACCGTTTAAGACGATTTACAGATTCA 324
 QY 111 ThrThrValLeuAlaAspThrValValAlaAlaThrGlyValAlaValAlaArgLeuHis 130
 Db 325 AAAGCCATTCTCGCTGACCTGTGATCTCGTACTGAGAGCTGTGGTAAAGCGGTTAGC 384
 QY 131 Phe-----SerGlySerAspThrThrTrpAsnArgGlyIleSerAlaCysAla 146
 Db 385 TTGCTTGGATCTGGTGAAGGTTCTGGAGGTTCTGGAACCGTGAATCTCCGCTTGCT 444
 QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166

Db 445 GTTTCGCGAGCGAGCTGCTCCGATATTCGTAACAAACCTCTTGGGTGATCGGTGAGGC 504
 QY 167 AspSerAlaMetGluGluGlyAsnPheLeuThrIleValThrGlySerGlnValThrIle 186
 Db 505 GATTCAGCAATGGAAGCAAACTTTCTTACAAATAATGATCTAAAGTGTATATAATC 564
 QY 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuSerAsnPro 206
 Db 565 CATAGGAGAGATGCTTTTAGAGCGCTTAAGATTATGACAGCAGCGAGCTTTGCTAATCCT 624
 QY 207 LysIleGlnValValTrpAspSerGluValValGluAlaThrGlyGlyAlaGlyGly 226
 Db 625 AAGATTGATGATTGGAACTCGTCTCTTGTGAAGCTTATGGAGATGGAGAAGAGAT 684
 QY 227 ProLeuAlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGlnVal 246
 Db 685 GTGCTTGGAGATTGAAAGTGAAGATGTGTTTACCGGAGATGTTTCTGATTTAAAGTT 744
 QY 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrIlePheLeuAsnGlyGlnLeu 266
 Db 745 TCTGATTTGTTCTTGTGTTGGTCAAGCAGCTACCAAGTTTGTGGATGGTGGTGT 804
 QY 267 GluLeuHisAlaAspGlyThrValAlaThrLysProGlySerThrHisThrSerValGlu 286
 Db 805 GAGTTAGATTCCGATGGTTATGTTGTACGAAGCTTGGTACTACACAGCTAGCGTCCC 864
 QY 287 GlyValPheAlaAlaGlyAspValGlnAspLysIleThrArgGlnAlaIleThrAlaAla 306
 Db 865 GGAGTTTTCGCTCGGGTGATGTTTCAGATTAAGATATAGGCAAGCCATCCTCCTGCA 924
 QY 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisThrLeuGlnGluValGlyAlaGln 326
 Db 925 GGAAGCTGGTGCATGGCAGCTTTGGATGCGAGCATTACTTACAGAGATTGGATCTCAG 984

RESULT 13

US-10-032-201B-10
 ; Sequence 10, Application US/10032201B
 ; Publication No. US20030167524A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Rooijen, Gijls
 ; APPLICANT: Deckers, Harm
 ; APPLICANT: Heifetz, Peter Bernard
 ; APPLICANT: Briggs, Steven
 ; APPLICANT: Dalmia, Bipin Kumar
 ; APPLICANT: Del Val, Greg
 ; APPLICANT: Zaplachinski, Steve
 ; APPLICANT: Moloney, Maurice
 ; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
 ; FILE REFERENCE: 38814 351B
 ; CURRENT APPLICATION NUMBER: US/10/032,201B
 ; CURRENT FILING DATE: 2001-12-19
 ; NUMBER OF SEQ ID NOS: 313
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10
 ; LENGTH: 1002
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1002)
 ; OTHER INFORMATION: cDNA encoding NADPH thioredoxin reductase
 ; US-10-032-201B-10

Alignment Scores:
 Pred. No.: 1.54e-157 Length: 1002
 Score: 1324.00 Matches: 252
 Percent Similarity: 88.00% Conservative: 34

Best Local Similarity: 77.54% Mismatches: 35
 Query Match: 77.61% Indels: 4
 DB: 15 Gaps: 1

US-10-091-841A-9 (1-332) x US-10-032-201B-10 (1-1002)

QY 11 ThrArgValCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
 DB 25 ACAAGGCTCTGTATCGTAGAGAGTGGCCCGGCGCACACACGGGGCGGATTTACGAGCT 84
 QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50
 DB 85 AGGCTGAACCTTAAACCTCTCTCTCGAAGATGGATGCTTAACGACATCGCTCCCGGT 144
 QY 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProThrGlyIleMet 70
 DB 145 GGTCACTAAACACACCGAGCTGAGATTTCCCGGATTTCCGAGAGTATTCTC 204
 QY 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
 DB 205 GGAGTAGAGCTCACTGACAAATTCGTAAACATCGGAGGATTCGGTACTACGATATT 264
 QY 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
 DB 265 ACAGAGCGGTGAGAGAGTGGATTTCTTCGAAACCGTTTAAGCTATTACAGATTCA 324
 QY 111 ThrThrValLeuAlaAspThrValValAlaThrGlyValAlaAlaArgArgLeuHis 130
 DB 325 AAAGCCATTCTCGTGAGCGTGTATTCGCTACTGAGCTGTGGCTAAGCGGCTTAGC 384
 QY 131 Phe-----SerGlySerAspThrTyrTrpAsnArgGlyIleSerAlaCysAla 146
 DB 385 TTCGTGGATCTGGTAGAGTTCGGAGGTTCTTGGAAACCGTGGAAATCTCCGCTTGCT 444
 QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyGly 166
 DB 445 GTTTGGACGAGCTGCTCCGATATTCGTAAACAACTCTTGGCGTATCGGTGGAGGC 504
 QY 167 AspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGlySerGlnValTyrIle 186
 DB 505 GATTTCAGCAATGGAAGAGCAAACTTTCTTACAAATATGATCTAAAGTGTATTAATC 564
 QY 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuSerAsnPro 206
 DB 565 CATAGGAGAGTCTTTAGAGCTCTTAAGATTATGACGACGAGCTTTGTCTAATCT 624
 QY 207 LysIleGlnValValTrpAspSerGluValValGluAlaTyrGlyAlaGlyGlyGly 226
 DB 625 AAGATTGATGATTGGAACTCTGCTGTTGTGAAGCTTATGGAGATGGAGAAAGAGAT 684
 QY 227 ProLeuAlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGlnVal 246
 DB 685 GTGCTTGAGGATTGAAGTGAAGATGTGGTTTACCGGAGATGTTCTGATTTAAAGTT 744
 QY 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeu 266
 DB 745 TCTGATTGTTCTTTGCTATTGGTTCATGAGCCAGCTACCAAGTTTGGATGGTGGT 804
 QY 267 GluLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerValGlu 286
 DB 805 GAGTTAGATTCCGATGGTATTGTTGTACGAAAGCTCGTACTACACAGACTAGCGTTCCC 864
 QY 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
 DB 865 GGAGTTTTCGTCGGGTGATGTTTCAGATTAAGATATAGGCAAGCCATCACTGCTGCA 924
 QY 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluValGlyAlaGln 326
 DB 925 GGAATGGGTGCATGGCAGCTTGGATGCAGAGCATTTACTTACAAGAGATGGATCTCAG 984
 QY 327 ValGlyLysSerAsp 331
 DB 985 CAAGTAAAGATGAT 999

RESULT 14

US-10-290-072-238
 ; Sequence 238, Application US/10290072
 ; Publication No. US20030211511A1
 ; GENERAL INFORMATION:

; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Dalmia, Bipin K.
 ; APPLICANT: del Val, Greg
 ; APPLICANT: Desjardis, John R.
 ; APPLICANT: Heifetz, Peter
 ; APPLICANT: Luginbuhl, Peter
 ; APPLICANT: Muchhal, Umesh

; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity

; FILE REFERENCE: A-71457-3

; CURRENT APPLICATION NUMBER: US/10/290,072

; CURRENT FILING DATE: 2002-11-06

; PRIOR APPLICATION NUMBER: US 60/370,609

; PRIOR FILING DATE: 2002-04-05

; PRIOR APPLICATION NUMBER: US 60/376,682

; PRIOR FILING DATE: 2002-04-29

; PRIOR APPLICATION NUMBER: US 10/141,531

; PRIOR FILING DATE: 2002-05-06

; PRIOR APPLICATION NUMBER: US 60/289,029

; PRIOR FILING DATE: 2001-05-04

; NUMBER OF SEQ ID NOS: 239

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 238

; LENGTH: 1344

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: synthetic

US-10-290-072-238

Alignment Scores:

Pred. No.: 2 37e-157 Length: 1344
 Score: 1324.00 Matches: 252
 Percent Similarity: 88.00% Conservative: 34
 Best Local Similarity: 77.54% Mismatches: 35
 Query Match: 77.61% Indels: 4
 DB: 13 Gaps: 1

US-10-091-841A-9 (1-332) x US-10-290-072-238 (1-1344)

QY 11 ThrArgValCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
 DB 367 ACAAGGCTCTGTATCGTAGAGTGGCCCGGCGCACACACGGCGGCGATTTACGAGCT 426
 QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50
 DB 427 AGGCTTGAACCTTAAACCTTCTTCGAGATGGATGGCTTAACGACATCGCTCCCGT 486
 QY 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProThrGlyIleMet 70
 DB 487 GGTCAACTAAACAACACCGAGCTCGAGATTTCCCGGATTTCCAGAAAGTATTCTC 546
 QY 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
 DB 547 GGATGATGATCACTGACAAATTCGTAACCAATCGGAGCGGATTCGGTACTACGATATT 606
 QY 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
 DB 607 ACAGAGCGGTGACGAAAGTCGATTTCTTCGAAACCGTTTAAGCTATTACAGATTCA 666
 QY 111 ThrThrValLeuAlaAspThrValValAlaThrGlyAlaValAlaArgArgLeuHis 130
 DB 667 AAAGCCATTCTCGCTGAGCTGTGATTTCTGCTACTGAGCTGTGGCTAAGCGGCTTAGC 726
 QY 131 Phe-----SerGlySerAspThrTyrTrpAsnArgGlyIleSerAlaCysAla 146
 DB 727 TTCGTGGATCTGGTGAAGTTCTGGAACCGTGGATCTCCGCTTGTGCT 786


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Qy 267 GluLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerValGlu 286
Db 2359 GAGTTAGATTGGATGGTTATGTTGCACGAGCCTGGTACTACACAGACTAGCGTCCC 2418
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
Db 2419 GGAGTTTTCGCTGCGGGTGATGTTCAGGATAAGAGTATAGGCAAGCCATCACTGCTGCA 2478
Qy 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluValGlyAlaGln 326
Db 2479 GGAACCTGGGTGCATGGCAGCTTTGGATGCCAGACATTACTTACAGAGATTGGATCTCAG 2538
Qy 327 ValGlyLysSerAsp 331
Db 2539 CAAGGTAAGAGTGAT 2553
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Search completed: June 21, 2004, 21:10:34
Job time : 511 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2004, 18:37:01 ; Search time 89 Seconds
(without alignments)

2070.154 Million cell updates/sec

Title: US-10-091-841A-9

Perfect score: 1706

Sequence: 1 MEGSAAPLRTRVCIIIGSP.....ALDAEHLQEVGAQVGRSDZ 332

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool/US10091841/runat_21062004_163837_28587/app_query.fasta_1.519
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B COMB.seq:*

3: /cgn2_6/ptodata/2/ina/5A COMB.seq:*

4: /cgn2_6/ptodata/2/ina/5B COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PTCUS COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1628	95.4	995	4	US-09-540-014-10
2	1628	95.4	995	4	US-09-540-014-23
3	1469	86.1	1560	4	US-09-598-747-26
4	1296	76.0	1021	4	US-09-598-747-24
5	1223.5	71.7	998	4	US-09-540-014-26
6	910.5	53.4	1230025	4	US-09-198-452A-1
7	895.5	52.5	1423	1	US-08-386-729A-6
8	720	42.8	1443	1	US-09-221-017S-685
9	723	42.4	4403765	3	US-09-103-840A-2
10	723	42.4	4411529	3	US-09-103-840A-1
11	707.5	41.5	963	4	US-09-328-352-1552
12	707.5	41.5	49617	4	US-09-596-002-28

Alignment Scores:

Pred. No.: 2.5e-178 Length: 995
Score: 1628.00 Matches: 328
Percent Similarity: 98.80% Conservative: 0
Best Local Similarity: 98.80% Mismatches: 3

ALIGNMENTS

RESULT 1

US-09-540-014-10

; Sequence 10, Application US/09540014

; Patent No. 6380372

; GENERAL INFORMATION:

; APPLICANT: Cho, Myeong-Je

; APPLICANT: Del Val, Greg

; APPLICANT: Caillau, Maxime

; APPLICANT: Lemauz, Peggy G.

; APPLICANT: Buchanan, Bob B.

; TITLE OF INVENTION: Barley Gene for Thioedoxin and

; TITLE OF INVENTION: NADP-Thioedoxin Reductase

; FILE REFERENCE: 2001-0701.30

; CURRENT APPLICATION NUMBER: US/09/540,014

; CURRENT FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: US 60/127,198

; PRIOR FILING DATE: 1999-03-31

; PRIOR APPLICATION NUMBER: US 60/169,162

; PRIOR FILING DATE: 1999-12-06

; PRIOR APPLICATION NUMBER: US 60/177,740

; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: US 60/177,739

; PRIOR FILING DATE: 2000-01-21

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10

; LENGTH: 995

; TYPE: DNA

; ORGANISM: Hordeum vulgare

US-09-540-014-10

Query Match: 95.43% Indels: 3
DB: 4 Gaps: 0

US-10-091-841A-9 (1-332) x US-09-540-014-10 (1-995)

QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgValCysIlelleGlySerGlyPro 20
DB 1 ATGAGGGATCCCGCGCGCGCGCTCCGACGCGGTGTGCATCATCGCAGCGCGCCG 60
QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
DB 61 GCCGCGCACAGCGCGCATCTACGCGCGCGCGCGGAGTCAAGCGGTCTTCGAG 120
QY 41 GlyTTPMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60
DB 121 GGCTGGATGGCCACAGCATCTCCGCGCGCGCGCGGAGTCAAGCGGTCTTCGAG 120
QY 61 AsnPheProGlyPheProThrGlyLeuMetGlyLeuAspLeuMetAspAsnCysArgAla 80
DB 181 AACTTCCCGGATTCCTCCACCGCATCTGGGATCGACCTCATGGACACTCCCGCGCC 240
QY 81 GlnSerValArgPheGlyThrAsnIleLeuSerGluThrValThrGluValAspPheSer 100
DB 241 CAGTCCGTCCGCTTCGCGACCAATCTCTCCGAGACCGTCCACCGAGGTCTCTCC 300
QY 101 AlaArgProPheArgValThrSerAspSerThrThrValLeuAlaAspThrValVal 120
DB 301 GCCCGCCCTTCGCGTCACTCCGATCTCCACACCGTCTCCGCGACCGGTCTCGTC 360
QY 121 AlaThrGlyAlaValAlaArgLeuHisPheSerGlySerAspThrTyrTrpAsnArg 140
DB 361 GCCACGGCGCGCGCGCGCGCTCCATTTCTCCGTTCCGACACTTACTGGAACCGC 420
QY 141 GlyTleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
DB 421 GGCATCTCCCGCTCCGCGCTCGCGCGCGCTCGCGCGCATCTTCGGACACAGCCCATC 480
QY 161 AlaValIleGlyGlyAspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGly 180
DB 481 GCCGTCACTCGCGCGCGGTGATTCGCCCATCGAGAGGCAACTTCTCCACCAAGTACGGA 540
QY 181 SerGlnValTyrIlelleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
DB 541 TCCCAAGTGATCATCATCCACGGCGCGCAACACTTCCGCGCTCCCAAGATTATGACGGCT 600
QY 201 ArgAlaLeuSerAsnProLysIleGlnValValTyrAspSerGluValValGluAlaTyr 220
DB 601 AGGCGCTCTCCAATCTTAAGATCCAGTTGTCTGGGACTC-CAGGTCTCGAGGCTTAC 659
QY 221 GlyGlyAlaGlyGlyProLeuAlaGlyValLysValLysAsnLeuValThrGlyGlu 240
DB 660 GCGCGTGCAGCGCGCGCGCCCATTAGCTGGGGTCAAGGTCAAGAACTTGGTGACTGTGAG 719
QY 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
DB 720 GTGTCTGACCTTCAGGTGTCCGGCTTTCTTCGCCATCGGCGATGAGCGCGGCCACCAAG 779
QY 261 PheLeuAsnGlyGlnLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGlySer 280
DB 780 TTTCTCAATGGGAGCTTGGCTTCATTCGCGATGGGTGTGTGGCCACCAAGCGCGCTCT 839
QY 281 ThrHisThrSerValGluGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg 300
DB 840 ACATATACCAAGTGTGGAGGGGTC-TTTGCTGTGGAGACGTGCAGGATTAAGAGTATCGT 898
QY 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu-AspAlaGluHisTyrLe 320
DB 899 CAGGCCATTACTGCTGTGATCAGGTGATGGCTGTCTTTGGACCGCGGACCTATCTCT 958
QY 320 uGlnGluValGlyValGlnValGlyLysSerAsp 331
DB 959 GCAGGAGTGGGTGCACAGGTGGGCAAGTCTGAT 992

RESULT 2

US-09-540-014-23
Sequence 23, Application US/09540014
Patent No. 6380372
GENERAL INFORMATION:
APPLICANT: Cho, Myeong-Je
APPLICANT: Del Val, Greg
APPLICANT: Caillaud, Maxime
APPLICANT: Lemaux, Peggy G.
APPLICANT: Buchanan, Bob B.
TITLE OF INVENTION: Barley Gene for Thioresdoxin and
TITLE OF INVENTION: NADP-Thioresdoxin Reductase
FILE REFERENCE: 2001-0701.30
CURRENT APPLICATION NUMBER: US/09/540,014
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 60/127,198
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: US 60/169,162
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 60/177,740
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 60/177,739
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 995
TYPE: DNA
ORGANISM: Hordeum vulgare
US-09-540-014-23

Alignment Scores:
Pred. No.: 2,58-178 Length: 995
Score: 1628.00 Matches: 328
Percent Similarity: 98.80% Conservative: 0
Best Local Similarity: 98.80% Mismatches: 3
Query Match: 95.43% Indels: 3
DB: 4 Gaps: 0

US-10-091-841A-9 (1-332) x US-09-540-014-23 (1-995)

QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgValCysIlelleGlySerGlyPro 20
DB 1 ATGAGGGATCCCGCGCGCGCGCTCCGACGCGGTGTGCATCATCGCAGCGCGCCG 60
QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
DB 61 GCCGCGCACAGCGCGCATCTACGCGCGCGCGGAGTCAAGCGGTCTTCGAG 120
QY 41 GlyTTPMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60
DB 121 GGCTGGATGGCCACAGCATCTCCGCGCGCGCGGAGTCAAGCGGTCTTCGAG 180
QY 61 AsnPheProGlyPheProThrGlyLeuMetGlyLeuAspLeuMetAspAsnCysArgAla 80
DB 181 AACTTCCCGGATTCCTCCACCGCATCTCCGAGACCGTCCACCGAGGTCTTCGAG 240
QY 81 GlnSerValArgPheGlyThrAsnIleLeuSerGluThrValThrGluValAspPheSer 100
DB 241 CAGTCCGTCCGCTTCGCGACCAATCTCTCCGAGACCGTCCACCGAGGTCTTCGAG 300
QY 101 AlaArgProPheArgValThrSerAspSerThrThrValLeuAlaAspThrValVal 120
DB 301 GCCCGCCCTTCGCGGTCACTCCGACTCCACCGCTCTCCGCGACACCGTCTCGTC 360
QY 121 AlaThrGlyAlaValAlaArgArgLeuHisPheSerGlySerAspThrTyrTrpAsnArg 140
DB 361 GCCACGGCGCGCGTCCGCGCGCTCCATTTCTCCGTTCCGACACTTACTGGAACCGC 420
QY 141 GlyTleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
DB 421 GGCATCTCCGCTCGCGCTCTGCAGCGCGGTCTGCAGCGCGGTCTTCGCGAACAGCCATC 480

QY 161 AlavallieGlyGlyAspSerAlaMetGluGluGlyAenPheLeuThrLysTyrGly 180
Db 481 GCCGTCATCGCGCGGCGGATTCGCCCATGAGAGGCAACTTCTCCACCAAGTACGGA 540
QY 181 SerGlnValTyrIleIleHisArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db 541 TCCCAAGTGATCATCATCCACGGGCGCAACACCTTCGCGGCTCCAAGATTATGACGGCT 600
QY 201 ArgAlaLeuSerAsnProLysIleGlnValValTyrAspSerGluValValGluAlaTyr 220
Db 601 AGGGCGCTCTCCAACTCCCTAAGATCCAGGTTCCTGCTGGGACTC-GAGGTCTGAGGCTTAC 659
QY 221 GlyGlyAlaGlyGlyGlyProLeuAlaGlyValLysValLysValLysValLysValLysVal 240
Db 660 GCGGTGTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 719
QY 241 ValSerAspLeuGlnValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLys 260
Db 720 GTGCTGACCTTCAGGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 779
QY 261 PheLeuAenGlyGlnLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGlySer 280
Db 780 TTTCATATGGGCACTTGAGCTCCATCCGATGCGGATGCGGCGGCGGCGGCGGCGGCGGCT 839
QY 281 ThrHisThrSerValGluGlyValPheAlaIleGlyAspValGlnAspLysTyrArg 300
Db 840 ACACATACAGGTTCGAGGCGGTC-TTTCGCTGCGGAGACGTCGAGGATAAGAGTATCGT 898
QY 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu-AspAlaGluHisTyrLe 320
Db 899 CAGGCGCATTACGCTGCTGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 958
QY 320 uGlnGluValGlyAlaGlnValGlyLysSerAsp 331
Db 959 GCAGGAGGTGGGTGCACAGGTGGGCAAGTCTCAT 992

RESULT 3
US-09-598-747-26
; Sequence 26, Application US/09598747
; Patent No. 6531648
; GENERAL INFORMATION:
; APPLICANT: Lananhan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gasdaska, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; FILE REFERENCE: A-31383PI
; CURRENT APPLICATION NUMBER: US/09/598,747
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-598-747-26

Alignment Scores:
Pred. No.: 1,13e-159 Length: 1560
Score: 1469.00 Matches: 283
Percent Similarity: 95.47% Conservative: 12
Best Local Similarity: 91.59% Mismatches: 14
Query Match: 86.11% Indels: 0
DB: 4 Gaps: 0

US-10-091-841A-9 (1-332) x US-09-598-747-26 (1-1560)

QY 1 MetGluGlySerAlaAlaAlaProLeuAthrArgValCysIleIleGlySerGlyPro 20
Db 406 ATGAGGAGTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 465
QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
:::|||||

Db 466 TCGCGGCAACACGCGGCGGCGGATCTACGCCGCGCGCGGAGCTCAAGCCCGTGTCTCTCGAG 525
QY 41 GlyTrpMetAlaAsnAspIleAlaIleGlyGlnLeuThrThrThrThrThrThrThrThrThrThr 60
526 GCGTGGCTCGCCCAAGACATCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 585
QY 61 AsnPheProGlyPheProThrGlyIleMetGlyIleAspLeuMetAspAsnCysArgAla 80
586 AACTTCCCGGGTTCCTCCGAGGGGATCTCCGCGGCGGAGCTCATGGATCGGTGCGCGCGC 645
QY 81 GlnSerValArgPheGlyThrAsnIleLeuSerGluThrValThrGluValAspPheSer 100
646 CAGTCCCTCCGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 705
QY 101 AlaArgProPheArgValThrSerAspSerThrThrValLeuAlaAspThrValValVal 120
706 GCGCGGCGGCTTCGCGGTTCGCTCCGACTCCACCGGTCTCCGCGGCGGCGGCGGCGGCGGCGG 765
QY 121 AlaThrGlyAlaValAlaArgArgLeuHisPheSerGlySerAspThrTyrTrpAsnArg 140
766 GCCACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 825
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
826 GGCATCTTCAGCTTCGCGGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 885
QY 161 AlaValIleGlyGlyAspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGly 180
886 GCGGTTCATCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 945
QY 181 SerGlnValTyrIleIleHisArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
946 TCCCATGTGTACATCATCCACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1005
QY 201 ArgAlaLeuSerAsnProLysIleGlnValValTyrAspSerGluValValGluAlaTyr 220
1006 AGGCGGTTCGCAACCCCAAGATCCAGGTTTCTCGGAGCTCTGAGGTCTGCGGAGGCGCTAC 1065
QY 221 GlyGlyAlaGlyGlyGlyProLeuAlaGlyValLysValLysValLysValLysValLysVal 240
1066 GCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1125
QY 241 ValSerAspLeuGlnValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLys 260
1126 ATCTCCGACCTTCAGGTTCGCGGTCTCTCTTCGCGCATCGACATGAACCGCGCGGCGGAG 1185
QY 261 PheLeuAsnGlyGlnLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGlySer 280
1186 TTTCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1245
QY 281 ThrHisThrSerValGluGlyValPheAlaAlaGlyAspValGlnAspLysTyrArg 300
1246 AGGCACACAGGTGTGAAGGGGCTCTTTGCTGCTGGGAGTGTGCGGAGACAGAGATATCGC 1305
QY 301 GlnAlaIleThrAlaAlaGlySerGly 309
Db 1306 CAGGCTATTACTGCGGCTGGATCAGGT 1332

RESULT 4
US-09-598-747-24
; Sequence 24, Application US/09598747
; Patent No. 6531648
; GENERAL INFORMATION:
; APPLICANT: Lananhan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gasdaska, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; FILE REFERENCE: A-31383PI
; CURRENT APPLICATION NUMBER: US/09/598,747
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1

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; SEQ ID NO 24
; LENGTH: 1021
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-598-747-24

Alignment Scores:
  5.41e-140      Length: 1021
  1296.00        Matches: 249
  86.77%         Conservative: 33
  76.62%         Mismatches: 39
  75.97%         Indels: 4
  4              Gaps: 1
DB:

US-10-091-841A-9 (1-332) x US-09-598-747-24 (1-1021)

QY 11 ThrArgValCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
DB 34 ACCGGCTCTGATCGTGGTTCGGCCCGGCTGCCACACCGCGGCATCTACGGCGCC 93
QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 50
DB 94 CGCGCGAGCTCAAGCGCTCTCTTCAGGGCTGGATGGCCACGACATCGCCCGCGC 153
QY 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProThrGlyIleMet 70
DB 154 GGCAGCTCACACACACCGAGCTGGAGAACTTCCCGGCTTCCCGAGGGCATCTTC 213
QY 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
DB 214 GCGGTGGAGCTGACCGACAAAGTTCGCAAGCAGCAGCGCGCTTCGGCACCACCATCTTC 273
QY 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
DB 274 ACCGAGCCGTCACCAAGTGAGCTTCGAGCAGCGCTTCAGCTCTTCACGAGCTCC 333
QY 111 ThrThrValLeuAlaAspThrValValAlaThrGlyAlaValAlaAlaArgArgLeuHis 130
DB 334 AAGGCATCTTCGGCGACGCGTGTATCTCCGCTCCGCGCGCTGCGCAAGTGGCTCTCC 393
QY 131 PheSerGlySerAspThr-----TyrTrpAsnArgGlyIleSerAlaCysAla 146
DB 394 TTCGTGGCTCTCGCGAGTCTCGGGCGCTCTGGAAACCGCGCATCTCCGCTCGGCT 453
QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
DB 454 GTGTGGCAGCGCGCGCCCGATCTTCGCAACAGCGCTCGCTGTGATCGGTGGCGGA 513
QY 167 AspSerAlaMetGluGluGlyAsnPheLeuThrIlystYrGlySerGlnValTyrIleIle 186
DB 514 GACAGCGCATGGAGGAGGCGCAACTTCTCCACCAAGTACGCTCCAAAGGTGTATCATCATC 573
QY 187 HisArgArgAsnThrPheArgAlaSerIlystIleMetGlnAlaArgAlaLeuSerAsnPro 206
DB 574 GACCGCGCGAGCGCTTCGGCGCTCCAGATCATGAGCAGCGCGCGCTCTCCACCCG 633
QY 207 LysIleGlnValValTrpAspSerGluValValGluAlaTyrGlyAlaGlyGlyGly 226
DB 634 AAGATCGACGTCATCTGGAACCTCTCGTGTGGAGGCTACGCGCAGCGCGCGCGAC 693
QY 227 ProLeuAlaGlyValLysValAsnLeuValThrGlyGluValSerAspLeuGlnVal 246
DB 694 GTGCTCGCGGCTCAAGTGAGAAAGCTGTGTGACCGCGAGCTGTCTCGACCTCAAGTG 753
QY 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeu 266
DB 754 TCCGCGCTCTTCTTCGCCATCGGCGACAGCGCGGCCCAAGTTCCTTCGACGCGCGCGT 813
QY 267 GlnLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerValGlu 286
DB 814 GAGCTGGACTCCGAGCGCTAGTGTGACCAAGCGCGCGCGCCACCCAGACCTCCGTGCTC 873
QY 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
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874 GCGGTGTTTCGCGCGCGCGAGCGTGCAGGACAAAGATACCGCCAGGCATCACCGCCGCC 933
307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluValGlyAlaGln 326
934 GGCACCGGCTGCATGGCGCGCTCGACCGCCGAGCATTACCTCCAGGAGATCGGTCTCCAG 993
327 ValGlyLysSerAsp 331
994 CAGGCGCAAGTCGGAC 1008

RESULT 5
US-09-540-014-26
; Sequence 26, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: NADP-Thioredoxin and
; TITLE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; PRIOR FILING DATE: 2000-03-31
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-540-014-26

Alignment Scores:
  1.22e-131      Length: 998
  1223.50        Matches: 242
  84.62%         Conservative: 33
  74.46%         Mismatches: 45
  71.72%         Indels: 6
  4              Gaps: 2
DB:

US-10-091-841A-9 (1-332) x US-09-540-014-26 (1-998)

QY 11 ThrArgValCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
DB 25 ACAAGCTCTGTATCGTAGGAGTGGCCCGGCGCACACGCGCGCATCTTACGACGT 84
QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 50
DB 85 AGCGGTGAACATAAACCTCTTCTCTCGAAGATGGATGGCTAACGACATCGCTCCCGGT 144
QY 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProThrGlyIleMet 70
DB 145 GGTCAACTCAACCAACACCGCGGT---GAGAAATTTCCCGGATTTCCAGAGGTATTCTC 201
QY 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
DB 202 GGAGTAGAGCTCACTGACAAATTCGTAACATCGGAGCGATTCGGTACTACGATATT 261
QY 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
DB 262 ACAGAGACGGTGACAAAAGTGATTTCTTCTCGAAACCGTTTAAAGCTATTACAGATTCA 321
QY 111 ThrThrValLeuAlaAspThrValValAlaThrGlyAlaValAlaAlaArgArgLeuHis 130
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Db 322 AAAGCATTCTCGCTGACCGCTGATCTCGCTATCGGAGCTGTGCTAAGTGGCTTAGC 381
QY 131 PheSerGlySerAspThr-----TyrTrpAsnArgGlyIleSerAlaCysAla 146
Db 382 TTGGTTGGATCTGGTGAAGTCTCGGAGGTTTGTGGACCGTGAATCTCCGCTGTGCT 441
QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
Db 442 GTTTCGAGCGAGCTGCTCCGATATTCGCAACAACCTCTTGGCGTATCGGTGGAGGC 501
QY 167 AspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGlySerGlnValTyrIleIle 186
Db 502 GATTCGCAATCGAAGACCAACTTCTTACAAATATGGATCTAAAGTGTATATAATC 561
QY 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuSerAsnPro 206
Db 562 GATAGAGAGATGCTTTTATAGCGCTTAAGATTTATGCAGCAGCT-TTGTCTAATCCT 620
QY 207 LysIleGlnValValTrpAspSerGluValValGluAlaTyrGlyAlaGlyGly 226
Db 621 AAGATTGATGTGATTGGAACTCGTCTGTGTGGAGCTTATGGAGATGGAGAAAGAGAT 680
QY 227 ProLeuAlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGlnVal 246
Db 681 GTGCTTGGAGGATTTGAAGTGAAGATGTGTGTACCGGAGATGTTCTGATTAAAGTT 740
QY 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeu 266
Db 741 TCTGGATTGTTCTTCTGCTATTGCTATGTCATGAGCAGCTACCAAGTTTGGATGGTGTGT 800
QY 267 GluLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerValGlu 286
Db 801 GAGTTAGATTGGATGGTGTATGTTGTACGAAAGCTGTGTACTACACAGACTAGCGTCCC 860
QY 287 GlyValPheAlaAlaGlyAspValGlnAspLysTyrArgGlnAlaThrAlaAla 306
Db 861 GAGTTTTCGTCGGGTGATGTTTCAGGATAGAAGTATAGGACGCCATCACTGCTGCA 920
QY 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluValGlyAlaGln 326
Db 921 GGAACGTGGTGTCAGTGGCAGCTTTGGATTCAGAGCATTACTTACAGAGATTGGATCTCAG 980
QY 327 ValGlyLysSerAsp 331
Db 981 CAAGGTAAGATGAT 995

RESULT 6
US-09-198-452A-1/c
; Sequence 1, Application US/09198452A
; Patent No. 655294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE OF INVENTION: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(15000)
; OTHER INFORMATION: n=a or c or g or t
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; OTHER INFORMATION: n=a or c or g or t
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; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (390001)..(405000)
; OTHER INFORMATION: n=a or c or g or t
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QY	9	LeuArgThrArgValCysIlelleGlySerGlyProAlaAlaHisThrAlaIleTy	28
Db	366596	ATTCATTCCTCCGGTTAAATATTTATTTGGTTACGTCATACAGCGCAATTTAT	366537
QY	29	AlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTirpMetAlaAsnAspIleAla	48
Db	366536	GCATCAGAGCGCTTTGCATCTCTTTATTTGAGGGGTTTTCCTCTGGG-----ATC	366483
QY	49	AlaGlyGlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProThrGly	68
Db	366482	TCTGTGGCCAGCTTATGACTACACAGAAGTTTGAGAAATTTTCCAGGGTTTCTCGAAGG	366423
QY	69	IleMetGlyIleAspLeuMetAspAsnCyseArgAlaGlnSerValArgPheGlyThrAsn	88
Db	366422	ATTCITGGGCCAAACCTATGAATAATATGAAGAGCAGCGCTGTGGGTTTGGGACCAAG	366363
QY	89	IleLeuSerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSer	108
Db	366362	ACACTAGCTCAAGATATTTATTTCCGTAGATTTTCTGTTCCGCCCTTTTATTTGAAATCA	366303
QY	109	AspSerThrThrValLeuAlaAspThrValValAlaAlaThrGlyAlaValAlaArgArg	128
Db	366302	AAAGAAGAAACCTATTCTTGTGATGCCTGTATCATGACTACAGAGCTTCTGCTAAACGT	366243
QY	129	LeuHisPhe-----SerGlySerAspThrTyTirpAsnArgGlyIleSerAlaCySAla	146
Db	366242	TTAGAAATTCCTGGAGCAGGAACGATGATTTTGGCAAAAGAGTGACTGCTGTGGCC	366183
QY	147	ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyGly	166
Db	366182	GTTCGCATGGGGCTTCTCTATTTTAAAAATAAGATCTTTATCTGATTTGGGAGGGG	366123


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Db 463 TCCAGCTTGACCTCTCTCCGCGCCCTTCAAGATGTGGACCGAGTGGACGATGACGAA 522
Qy 110 -----SerThrValLeuAlaAspThrValValValAlaThrGlyAlaValAlaArg 127
Db 523 GGCAGCGAGCCGCTCGCCAGCGCCGCGCTCATTCATTCAGCGAGCGCCAGCGCCG 582
Qy 128 ArgLeuHisPheSerGlySerAspThrThrTrpAsnArgGlyIleSerAlaCysAlaVal 147
Db 593 CQTCTGAACCTGCGCGGAGGAGGACCTCTGGCAGACGGAATCAGCGCTGTGCGTC 642
Qy 148 CysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyAsp 167
Db 643 TGCAGCGGTGCGTCCCTCCCTTCCGTAACAGCCCTGTACGTCAITGGCGGTGGTGC 702
Qy 168 SerAlaMetGluGluGlyAsnPheLeuThrLysTrpGlySerGlnValTyrIleIleHis 187
Db 703 TCCGCGCGGAGGAGGACCATGTTCTTGGCAAGTACGACAGCGGTGCTCTCTGTT 762
Qy 188 ArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuSerAsnProLys 207
Db 763 CGCAAGGACAGCTCGGTGCTCTTAAACATCATGCTGATGCTCTCTTGCACCCCAAG 822
Qy 208 IleGlnValValTrpAspSerLysValValGluAlaTyrGly---GlyAlaGlyGly 226
Db 823 TGCAGGTGCGCTTCAACACCGTCCACCGAGGTATTCGCGGAGAACACACCTAACGCG 882
Qy 227 ProLeuAlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGlnVal 246
Db 883 CTCATGACCCACCTCCGTTCAAGACGCTTCTCTAACCGGAGGAGGTGCTGAGGCT 942
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyLeu 266
Db 943 AACGCTCTCTTCTACGCTGTGGTTCAGCAGCCCGCCAGTGTCTGTCGTAAGGGCCAGGT 1002
Qy 267 GluLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerValGlu 286
Db 1003 GAGCTCGACGAGGAGATACATCATCACCAAGCCGCTACTAGCTTCACTAACGTCGAG 1062
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
Db 1063 GGTGTTTTGCGCTGCGGTGATGTTCCAGATAAGCGTACCGTACGCTATCACCAGTGC- 1121
Qy 306 ----- 306
Db 1122 CGTATGTTTACTTACCATCTCATTCATGATGATGCAATTTGGTCACTCAATATT 1181
Qy 307 -----GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGlu 322
Db 1182 CTACAGGATCTGGTGTGTGCTGCTCTCTTGGGCTGAGAGTTTCATCGCGAG 1235

RESULT 8
US-09-221-017B-685/c
; Sequence 685, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Monroy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 685:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1443 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1...1443
US-09-221-017B-685

Alignment Scores:
Pred. No.: 1,95e-74 Length: 1443
Score: 730.00 Matches: 154
Percent Similarity: 62.97% Conservative: 45
Best Local Similarity: 48.73% Mismatches: 105
Query Match: 42.79% Indels: 12
DB: 4 Gaps: 5

US-10-091-841A-9 (1-332) x US-09-221-017B-685 (1-1443)
Qy 12 ArgValCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAlaArg 31
Db 1189 CGCTGTCTCATCATCGTTCCGACCTCGCGGTATACCGCAGCTATCTATGCTTCTCGT 1130
Qy 32 AlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaGlyGly 51
Db 1129 GCCAACCCTCAACCCCATCTCTACGAGGG-----ATCAACCCGCGGT 1085
Qy 52 GlnLeuThrThrThrAspValGluAsnPheProGlyPheProGlyIleMetGly 71
Db 1084 CAGCTAACGACTACGACCGAGGTGGAAACTTCCCGGGTTATCCGAGGAATCACCGGT 1025
Qy 72 IleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeuSer 91
Db 1024 ACGGAACCTGATGGAACCTCGCAACCAAGCCGCTTCGGAGCGGACATTCGTTCCG 965
Qy 92 GluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAsp---Ser 110
Db 964 GGTATCGCTACAAAGCGGATTGAGCAAGGCTCTTACAGGATCAGCATAGACGGAGAA 905
Qy 111 ThrThrValLeuAlaAspThrValValAlaThrGlyAlaValAlaArgLeuHis 130
Db 904 AAGGAATACAGCCGATACGTTTATCTCCAGGGTGCACAGCCCAATCTTAGGC 845
Qy 131 PheSerGlySerAspThrTyrTrpAsnArgGlyIleSerAlaCysAlaValCysAspGly 150
Db 131 PheSerGlySerAspThrTyrTrpAsnArgGlyIleSerAlaCysAlaValCysAspGly 150
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844	TTGGCCGATGAAGCCAAATATATCCCGGCATGGGTGTTTCTGCTGTGTGCTACCTGTGTGATGGA	785
151	AlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyGlyAspSerAlaMet	170
784	TTT-----TTCTCGCAAGAAAGAACTACCGCTAGTGGCGGAGGTGATATGCTTGC	731
171	GlulGluGlyAsnPheLeuThrIlySerGlySerGlnValTyrIleIleHisArgArgAsn	190
730	GAGGAGGCTCTTATCTGGCATCGCTGGCTGAAACACGTGTACTCTGATCGTACGCAAGAAC	671
191	ThrPheArgAlaSerIlyMetGlnAlaArgAlaLeuSerAsnProLysIleGlnVal	210
670	TATCTCCGTCCCTCCAAAGTAAATGACGAGCGGTGTGATGAATACGGCGCAACATAACCGTT	611
211	ValTrpAspSerGluValValGluAlaTyrGly-----GlyAlaGlyGlyGlyProLeu	228
610	CTCTTCGAACATAAATACCGTGGTCTATTTCGGCGAAACGGTGTGGAGGTGCTCATCTG	551
229	AlaGlyValIlyValIlyAsnLeuValThrGlyGluValSerAspLeuGlnValSerGly	248
550	-----GTGAACGCAAAAGAGAGCGCGACGAGAGATGTTGCATTCGATGTT	497
249	LeuPhePheAlaIleGlyHisGluProAlaThrIlyPheLeuAsnGlyGlnLeuGluLeu	268
496	TTTTTCTCGCTATCGTTCATACGCCAACTCGAAGATCTTCGGCGACTTCTCGACTTG	437
269	HisAlaAspGlyTyrValAlaThrIlyProGlySerThrHisThrSerValGluGlyVal	288
436	GACGAAGTGGGTATATCTCTACGGAAGTTTCGTCCCGCGGCACAAAAGTTCCCGCGTA	377
289	PheAlaAlaGlyAspValGlnAspIlySlyTyrArgGlnAlaIleThrAlaAlaGlySer	308
376	TTTGTCCCGCGGAGTTGCCGCCACCACTATCTGTCAGCTATACAGGCTGCCGATCA	317
309	GlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluValGly	324
316	GGTTGCAAGCTTCTATCGAAGCAGAGCGTTATTATTGGCGGAGCAACCGT	269

RESULT 9

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RESULI' 9
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R. R. M.
; APPLICANT: FRASER, John C.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

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Db	4394860	AGCGGCGAGTGGCTGGCCCGCGGCTATCGACCGGAGCGCTGGCTCGCCGAG	---	CACGC	4394911
Qy	325	aGlnValGlyLysSerAsp	331		
Db	4394917	AGCAACCGAGAAGCTGAC	4394935		
RESULT 10					
US-09-103-840A-1					
; Sequence 1, Application US/09103840A					
; Patent No. 6294328					

Qy	8	ProLeuArgThrArg-ValCysIleIleIleGlySerGlyProAlaAlaHisThrAlaAlaI	27
Db	4393993	CCACCCCGTTCGCGAGCTGATCGTTATCGGCTCCGCGTCCGCGGGGTACACTCGCGCGT	4394052
Qy	27	eTyAlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspI	47
Db	4394053	CTACGCGCCGCTGCCAGCTGGCGCGCTGTCTTCGAGGCG-----AC	4394097
Qy	47	eAlaAlaGlyGlyGlnLeuThrThrThrThrAspValGluAsnPheProGlyPheProTh	67
Db	4394098	GTCTTTTCGCGCGCGCGCTGATGACCAACCCAGCTGGAGAACTACCCGGGATTCGCAA	4394157
Qy	67	xGlyIleMetGlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyTh	87
Db	4394158	CGSCATCACCGTCCAGAGTTGATGATGAGATCGGGAAAGCGGCTCGATTCGGCGC	4394217
Qy	87	rAnIleLeuSerGluThrValThrGluValAspPheSerAlaArgProPheArg-----	105
Db	4394218	GGACCTCGGTATGGAAAGCGTCGAGTCGTATCACTTCACGGG---CCGCTGAAATCGGT	4394274
Qy	106	-ValThrSerAspSerThrThrValLeuAlaAspThrValValAlaAlaThrGlyAlaVa	125
Db	4394275	CGTCACGCGCGGACAGACCCACCGGCGCGGCGGTGATCCTGGCAATGGCGCGACG	4394334
Qy	125	lAlaArgArgLeuHisPheSerGlySerAspThrTyrTrpAsnArgGlyIleSerAlaCy	145
Db	4394335	GGCACGCTATCTGCAAGTCCCGCGGAAACAGGAATTCGTCGCGCGCGGGGTGAGTCGTG	4394394
Qy	145	sAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGl	165
Db	4394395	CGCCACCTCGGCGGATTC-----TTCTTCGCGATCAGGACATCGCGTATCGCGCG	4394448
Qy	165	yGlyAspSerAlaMetGluGluGluGlyAsnPheLeuThrLysTyrGlySerGlnValTyrI	185
Db	4394449	CGGTGACTCGGCAATCGGAGAGACTACCTTCGTGACCCGATTCGTCGCGAGTGTGACGT	4394508
Qy	185	eIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuSerAs	205
Db	4394509	GGTGTCATCGCGCGAGAGTTCGGGCTTCCAAATCATGCTCGATCGCGCCCGCAACA	4394568
Qy	205	nProLysIleGlnValValTrpAspSerGluValValGluAlaTyrGlyGlyAlaGlyGl	225
Db	4394569	CGCAAGATACCGTTCCTCACAACACACCGTGTGCGGTGGAGCGGGGACACC-----	4394623
Qy	225	yGlyProLeuAlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGl	245
Db	4394624	---ACAGTGACCGGCTTCGGGTAGCGACACCAACCGGTGGCAACACCACTGCC	4394679
Qy	245	nValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGl	265
Db	4394680	GGTAACCGGTGTTTCGTTCGCATCGGCACGAGCGCGGTGCGGTGCGCGAGCG	4394739
Qy	265	nLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerVa	285
Db	4394740	CATCGAGCTCGACCGCGCTACGTGTGTGTGAGGGCGGTACCAACAGCACTCATC	4394799
Qy	285	lGluGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAl	305
Db	4394800	GCGCGCGGTGTTTCGTTCGCGCGGACCTGTGTGATCGCACTATCGCAGCGGTTACCGC	4394859
Qy	305	aAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluValGlyAl	325
Db	4394860	AGCGGCGAGTGGCTGGCGCGCGCTATCGACCGCGAGCGCTGGCTCGCGCGAG---	4394916
Qy	325	aGlnValGlyLysSerAsp	331
Db	4394917	AGCAACCGGAGAGCTGAC	4394935

DECEMBER 10

RESULT 10
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328

Qy	225	yGlyProLeuAlaGlyVallysVallysAsnLeuValThrGlyValValSerAspLeuG1	245
Db	4402388	-----ACAGTACCGCGTTCGGGTACGCGACCAACACCGGTGCGGACCAACCGTTCGC	4402443
Qy	245	nValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyG1	265
Db	4402444	GGTAAACCGGTGTTTTCGTCGGATCCGCCACGACCGCGTTCGGGTTCGGTTCGGCGAGGC	4402503
Qy	265	nLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerVa	285
Db	4402504	CATCGACGTCCGACCGCGTACGTGTGTGTCAGGCGGTATCCACGACGACCTCACT	4402563
Qy	285	lGluGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaThrAl	305
Db	4402564	GCGGCGGTTCGTCGCCGCGACCTGTGTGATCCACTATCCGACGCGGTTCACCG	4402623
Qy	305	aAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluValGlyAl	325
Db	4402624	AGCGGCGAGTGTTCGCGCGCTATCGACGCGGCTATCGCGGCTGCGTTCGCGAG--	4402680
Qy	325	aGlnValGlyLysSerAsp	331
Db	4402681	AGCAACCGGAGAGCTGAC	4402699
RESULT 11			
US-09-328-352-1552			
; Sequence 1552, Application US/09328352			
; Patent No. 8562958			
; GENERAL INFORMATION:			
; APPLICANT: Gary L. Breton et al.			
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER			
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS			
; FILE REFERENCE: GPC99-03PA			
; CURRENT APPLICATION NUMBER: US/09/328,352			
; CURRENT FILING DATE: 1999-06-04			
; NUMBER OF SEQ ID NOS: 8252			
; SEQ ID NO 1552			
; TYPE: DNA			
; ORGANISM: Acinetobacter baumannii			
US-09-328-352-1552			
Alignment Scores:			
Pred. No.: 4,11e-72 Length: 963			
Score: 707.50 Matches: 145			
Percent Similarity: 63.12% Conservative: 57			
Best Local Similarity: 45.31% Mismatches: 101			
Query Match: 41.47% Indels: 17			
DB: 4 Gaps: 6			
US-10-091-841A-9 (1-332) x US-09-328-352-1552 (1-963)			
Qy	11	ThrArgValCysIlelleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla	30
Db	31	TCTCGGTAAATATTCTCGGTCTCGCCCTCGGGTTATAGTCAGCTGTTATGCGACA	90
Qy	31	ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaGly	50
Db	91	CGTGCAATCTTAACCAACACTTATTTCAGGT-----TTACAGCTGGC	135
Qy	51	GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProGlyVileMet	70
Db	136	GGCCAACTTACACACACACCGAGTTGACACTGCGCGGCGCATCTGAGGTTTGACT	195
Qy	71	GlyIleAspLeuMetAspAsnCysA-GAlaGlnSerValArgPheGlyThrAsnIleLeu	90
Db	196	GGTCTCGCTTAATGACCGTATGCAAGCACATGCTGAACGCTTTCGTACCGAATGTC	255
Qy	91	SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer	110
Db	256	TATGACATTAATGAAGTGGACTTAAATGTACGTCCTTTTCTTAAAGGTGATATG	315
Qy	111	ThrThrValLeuAlaAspThrValValAlaThrGlyValAlaAlaArgArgLeuHis	130

Qy	225	yGlyProLeuAlaGlyVallysVallysAsnLeuValThrGlyValValSerAspLeuG1	245
Db	4402388	-----ACAGTACCGCGTTCGGGTACGCGACCAACACCGGTGCGGACCAACCGTTCGC	4402443
Qy	245	nValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyG1	265
Db	4402444	GGTAAACCGGTGTTTTCGTCGGATCGCCACGACCGCGTTCGGGTTCGGCGGAGGC	4402503
Qy	265	nLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerVa	285
Db	4402504	CATCGACGTGACCGCGACCGCTACGTGTGTGTCAGGCGGTATCCACGACCACTCACT	4402563
Qy	285	lGluGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaThrAl	305
Db	4402564	GCGGGCGGTTCGTCGCCGCGACCTGTGTGATCCACTATCGCAGCGGTATCCGC	4402623
Qy	305	aAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluValGlyAl	325
Db	4402624	AGCGGCGAGTGGCTGCGCGCGCTATCGACGCGCGCTGCTGCGGAG--CACGC	4402680
Qy	325	aGlnValGlyLysSerAsp	331
Db	4402681	AGCAACCGGAGAGCTGAC	4402699
RESULT 11			
US-09-328-352-1552			
; Sequence 1552, Application US/09328352			
; Patent No. 8562958			
; GENERAL INFORMATION:			
; APPLICANT: Gary L. Bretton et al.			
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER			
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS			
; FILE REFERENCE: GPC99-03PA			
; CURRENT APPLICATION NUMBER: US/09/328,352			
; CURRENT FILING DATE: 1999-06-04			
; NUMBER OF SEQ ID NOS: 8252			
; SEQ ID NO 1552			
; TYPE: DNA			
; ORGANISM: Acinetobacter baumannii			
US-09-328-352-1552			
Alignment Scores:			
Pred. No.: 4,11e-72 Length: 963			
Score: 707.50 Matches: 145			
Percent Similarity: 63.12% Conservative: 57			
Best Local Similarity: 45.31% Mismatches: 101			
Query Match: 41.47% Indels: 17			
DB: 4 Gaps: 6			
US-10-091-841A-9 (1-332) x US-09-328-352-1552 (1-963)			
Qy	11	ThrArgValCysIlelleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla	30
Db	31	TCTCGGTAAATATTCTCGGTCTGCGCTCGGGTATAGTCAGCTGTTATGCGACA	90
Qy	31	ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaGly	50
Db	91	CGTGCAATCTTAAACCAACACTTATTGAGGT-----TTACAGCTGGC	135
Qy	51	GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProGlyVileMet	70
Db	136	GGCCAACTTACACACACACCGAGTTGACACTGCGCGGCGCATCTGAGGTTTGACT	195
Qy	71	GlyIleAspLeuMetAspAsnCysA-GAlaGlnSerValArgPheGlyThrAsnIleLeu	90
Db	196	GGTCTCGCTTAATGACCGTATGCAAGCACATGCTGAAACGCTTTCGTACCGAATGTC	255
Qy	91	SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer	110
Db	256	TATGACATTAATGAAGTGGACTTAAATGTACGTCCTTTCTTAAAGGTGATATG	315
Qy	111	ThrThrValLeuAlaAspThrValValAlaThrGlyValAlaAlaArgArgLeuHis	130

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Db 316 GATGAGTACACTGTGATGCTTTAAATATTGCAACTGGTGCACAGCTCAATATCTTGGC 375
Qy 131 PheSerGlySerAspThrTyrTrpAsnArgGlyIleSerAlaCysAlaValCysAspGly 150
Db 376 TTAGAGTCTGAACAAATAATTATGGTCAAGCGGTGAGCGCATGTGCAACATGTGATGC 435
Qy 151 AlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyCysAspSerAlaMet 170
Db 436 TTC-----TTCACAAAGAACAAATGTGATGTTGGTGGTGGTAACTACTGCTGT 489
Qy 171 GluGluGlyAsnPheLeuThrLysTyrGlySerGlnValTyrIleIleHisArgArgAsn 190
Db 490 GAAGACAGCACTTTATTATCAATAATTTGCTGAACATGTGACATGTGACACCGCGCGAT 549
Qy 191 ThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuSerAsnPro-----Lys 207
Db 550 TCTTTACGCTCTGAGAAGATTTTACAGATCACTTTATTGCTAAAGAAAAAGAGCAGAA 609
Qy 208 IleGlnValValTrpAspSerGluValValGluAlaTyrGlyGlyAlaGlyGlyPro 227
Db 610 ATCAGTATCGTTTGGAAACCATGAGGTGAAGAGTTCTTGGTGACAATACTGCG----- 663
Qy 228 LeuAlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGlnValSer 247
Db 664 GTACAGGTGTTGCTTAAATCTACAAAGATGACAGCAACAAAGACAGTCTCAA 723
Qy 248 GlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeuGlu 267
Db 724 GCGTTATTCAATTCGCAATGCGCAATAAACCACCAATACCTCTATGTTTGAAGTCACTAAAT 783
Qy 268 LeuHisAlaAspGlyTyrValAlaThrLysProGly-----SerThrHisThr 283
Db 784 TTACGT---GATGGCTATATCCAGTACAAAGTGGTACTTCAGTTAACCAACAGGACT 840
Qy 284 SerValGluGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIle 303
Db 841 TCTGTACAGCGCTTTTGTGCTGCTGATGTTGCTGATGTTGCTGATGTTTATCTGTCAGCGATT 900
Qy 304 ThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluVal 323
Db 901 ACTTCGGCGGGTTTCAGGCTGTATGGTGCACATAGATGCCGAAATAATCTAGATAACCTT 960
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RESULT 12

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US-09-596-002-28/c
; Sequence 28, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 49617
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte template ID No. 6632636 28
; PUBLIC INFORMATION:
US-09-596-002-28
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Alignment Scores:

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Pred. No.: 1.89e-69 Length: 49617
Score: 707.50 Matches: 141
Percent Similarity: 63.30% Conservative: 66
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Best Local Similarity: 43.12% Mismatches: 103
Query Match: 41.47% Indels: 17
DB: 4 Gaps: 6
US-10-091-841A-9 (1-332) x US-09-596-002-28 (1-49617)
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Qy 4 SerAlaAlaProLeuArgThrArgValCysIleIleGlySerGlyProAlaAlaHis 23
Db 35473 AGTGCCTCTATGTACACAGCACCATCGCTTATCATTTCTGGCTCAGGCTCTCGAGGATAT 35414
Qy 24 ThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTrpMet 43
Db 35413 TCTCAGCGGTTTATGCGCGCGAGCTAACTCTAAACCCGCTCATTTATTACAGGC----- 35360
Qy 44 AlaAsnAspIleAlaAlaGlyGlnLeuThrThrThrThrAspValGluAsnPhePro 63
Db 35359 -----TTACAAGTTGGTGGACAGCTAACACCAACCAACCAAGTTGATACTAGTGCCA 35309
Qy 64 GlyPheProThrGlyIleMetGlyIleAspLeuMetAspAsnCysArgAlaGlnSerVal 83
Db 35308 GGTGATGCACATGTCTGACGGGCAACGGCTTATGAGGAGCAATGAATCCCATGCCGAA 35249
Qy 84 ArgPheGlyThrAsnIleLeuSerGluThrValThrGluValAspPheSerAlaArgPro 103
Db 35248 GCGTTTGGCACCAAGCTTATTATGACAGTATTACCCAGTTGATTACACAATCGCCCT 35189
Qy 104 PheArgValThrSerAspSerThrThrValLeuAlaAspThrValValAlaThrGly 123
Db 35188 TTTACGCTAGTGGCGATAAAGGTGCTATACCTGCGATCCCTTATTATTGTACAGGT 35129
Qy 124 AlaValAlaArgArgLeuHisPheSerGlySerAspThrTyrTrpAsnArgGlyIleSer 143
Db 35128 GCACCCGACAGTACCTAGGCTTGAATCTGAACAAAAGTTCATGGCTCAAGGTGTTCA 35069
Qy 144 AlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValle 163
Db 35068 GCATGTGCAACTGTGATGGCTTT-----TTTTATAAAATCAAAAGTCGCTGTTGTC 35015
Qy 164 GlyGlyGlyAspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGlySerGlnVal 183
Db 35014 GGTGGTGGTAAATACCGCTTTGAGAGGCTTATATTATTTATCAATATATCCAGGAGTT 34955
Qy 184 TyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeu 203
Db 34954 ACTTTGATACACCGCGAGATACTTTGCTGTCGCGCAAAAATACTACAAGACCAGTTATT 34895
Qy 204 SerAsnProLys-----IleGlnValValTrpAspSerGluValValGluAlaTyr 220
Db 34894 GAAAAGTTAAAGATGTAATATTATAATCGAATGGAAATCATCAATCAAAAGAGTCGT 34835
Qy 221 GlyGlyAlaGlyGlyProLeuAlaGlyValLysValLysAsnLeuValThrGlyGlu 240
Db 34834 GGTGATGACATGGC-----GTAACGGGGTTTATGATTGAGTCCACTCAAGATGGCTCA 34781
Qy 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db 34780 ATCAACACAGTTAGATATATTATGGTCTGTTGTCGCAATGGTCAATAACCAATACCAAG 34721
Qy 261 PheLeuAsnGlyGlnLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGly--- 279
Db 34720 TTATTGATGCTCAATTAATATGCAA--GATGATATATCTGTCACACGGGATTA 34664
Qy 280 -----SerThrHisThrSerValGluGlyValPheAlaAlaGlyAspValGlnAsp 296
Db 34663 AACGGCAATGCACAGCAACCAATCAATGGTGTGTTTTTCGCGTGGTGTGTTGTTGCTGAT 34604
Qy 297 LysLysTyrArgGlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAla 316
Db 34603 CACACCTATCGACAGGCAATCACTTCGCGAGGTAAGTCTGGCTGTATGGCTGCTGATGCC 34544
Qy 317 GluHisTyrLeuGlnGluVal 323
Db 34543 GAAAAGTATTATAGATTCACTT 34523
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Alignment Scores:	1.25e-65	Length:	1830121
Pred. No.:	695.50	Matches:	150
Score:	63.29%	Conservative:	50
Percent Similarity:	47.47%	Mismatches:	99
Best Local Similarity:	40.77%	Indels:	17
Query Match:	4	Gaps:	6
DB:			


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QY 12 ArgValCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAlaArg 31
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QY 32 AlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGlyGly 51
DB 1227844 GCAAACTTAAACACAGTATTTGGTGGT-----TTGCAACAGGTGGG 1227800
QY 52 GlnLeuThrThrThrThrValGluAsnPheProGlyPheProThrGlyIleMetGly 71
DB 1227799 CAGCTGACCACCTACAGATGAAATGAGAACTGCGCGCGCATTTTGGAGATGACTACTGGT 1227740
QY 72 IleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeuSer 91
DB 1227739 TCAGGTTTAAATGCAAGTATTTGCAACATGCAAGAAATTTGACACAGAAATCGTTTC 1227680
QY 92 GluThrValThrGluValAspPheSerAlaArgProPheArgPheGlyThrAsnIleLeuSer 91
DB 1227739 TCAGGTTTAAATGCAAGTATTTGCAACATGCAAGAAATTTGACACAGAAATCGTTTC 1227680
QY 92 GluThrValThrGluValAspPheSerAlaArgProPheArgPheGlyThrAsnIleLeuSer 111
DB 1227679 GATCATATCAATCGCTCGATTTATCTCTCGCCCATTCAAACTTTTGGCGATGTCGAA 1227620
QY 112 ThrValLeuAlaAspThrValValValAlaThrGlyAlaValAlaArgArgLeuHisPhe 131
DB 1227619 AATTTCATTGATGCGTTAATATTCGCAACAGGTGCTCTGCAAGTATATTCGGTTA 1227560
QY 132 SerGlySerAspThrTyrTrpAsnArgGlyIleSerAlaCysAlaValCysAspGlyAla 151
DB 1227559 CCTTCAGAGAAACTACAAAGTCTGCGCTTCTGCTGTGCAACCTGTGATGTTTC 1227500
QY 152 AlaProIlePheArgAsnLysProIleAlaValIleGlyGlyCysSerAlaMetGlu 171
DB 1227499 -----TTTTATCGTAATTAAGCTGTGCTGTCATGTTGGAGGAAATACACGCTGGAA 1227446
QY 172 GluGlyAsnPheLeuThrLysTyrGlySerGlnValTyrIleIleHisArgArgAsnThr 191
DB 1227445 GAAGCCCTTACTTAGCCATATTCGAACTACAGTGCATTTAATCCACGTCGCATAGC 1227386
QY 192 PheArgAlaSerLysIleMetGlnAlaArg-----AlaLeuSerAsnProLysIle 208
DB 1227385 TTCCGTGCGGAAAAATCCTTATCGATCCTTTATACAAAAAAGTGGAGAGGAAAAATC 1227326
QY 209 GlnValValTrpAspSerGluValValGluAlaTyrGlyGlyAlaGlyGlyGlyProLeu 228
DB 1227325 GTTCTTCATACACTGCGCACTTAGATGAATTTGCGGCAATATATGCGC-----GTA 1227272
QY 229 AlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGlnValSerGly 248
DB 1227271 ACTGGATTACGTTAGCCCAACAACTGCGGAGAGAAAGAACTCAAAATAGATGCGC 1227212
QY 249 LeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeuGluLeu 268
DB 1227211 TTATTCGTGCGGATTTGCTATTCGCAAAATACGAAATTTTCCAGGGGCACTAGAAATG 1227152
QY 269 HisAlaAspGlyTyrValAlaThrLysProGly-----SerThrHisThrSer 284
DB 1227151 AAT--AATGGCTATATCGTTGTAATCTGGTCTTGGCGCAATGCAACTGCCACTTCT 1227095
QY 285 ValGluGlyValPheAlaIleGlyAspValGlnAspLysLysTyrArgGlnAlaIleThr 304
DB 1227094 GTGGAAGGCGGTGTTCCGACAGCGCATGTCATGATGATCAAAATATGCGCAAGCCATTACC 1227035
QY 305 AlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeu 320
DB 1227034 TCCGCAAGAACTGTTGTTATGCGCGCTTGGATGCGAAGCGTATTTA 1226987

RESULT 15
US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
; Patent No. 6528289
; GENERAL INFORMATION:
; APPLICANT: Robert D. Fleischmann
; Mark D. Adams
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QY 112 ThrValLeuAlaAspThrValValValAlaThrGlyAlaValAlaArgArgLeuHisPhe 131
Db 1227619 AATTTCACTGTGTGATGCGTATTATTCGCAACAGGTGCTCTGCACGCTATATTGGCTTA 1227560
QY 132 SerGlySerAspThrTyTrpAsnArgGlyIleSerAlaCysAlaValCysAspGlyAla 151
Db 1227559 CTTTCAGAGAAGAACTACAAAGCTGTGGCGTCTCTGTGCAACCTGTGATGGTTTC 1227500
QY 152 AlaProIlePheArgAsnLysProIleAlaValIleGlyGlyValSpSerAlaMetGlu 171
Db 1227499 -----TTTATCGTAATAAGCTGTGTGTGTCATTGTGTGGAGGAATACAGCGGTGAA 1227446
QY 172 GluGlyAsnPheLeuThrLysTyGlySerGlnValTyIleIleHisArgAsnThr 191
Db 1227445 GAAGCCCTTTACTTACCCCAATATTCAGTACAGTCAATTTAATCCACCGTCGGATAGC 1227386
QY 192 PheArgAlaSerLysIleMetGlnAlaArg-----AlaLeuSerAsnProLysIle 208
Db 1227385 TTCCGTGCGGAAATAATCCTTATCGATCGTTATACAAAAAGTGGAGAGGGAATC 1227326
QY 209 GlnValValTrpAspSerGluValGluAlaTyGlyAlaGlyGlyProLeu 228
Db 1227325 GTTCTTCATACACTGACCGCACTTTAGATGAAGTATTGGGCGATAATATGCGC-----GTA 1227272
QY 229 AlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGlnValSerGly 248
Db 1227271 ACTGGATTACGTTAGCCACACAAAACTGGGGAGAGAGAACTCAATTAGATGCG 1227212
QY 249 LeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeuGluLeu 268
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QY 269 HisAlaAspGlyTyValAlaThrLysProGly-----SerThrHisThrSer 284
Db 1227151 AAT---AATGGCTATATCGTTGTAAATCTGGTCTTGACGGCAATGCACTGCCACTTCT 1227095
QY 285 ValGluGlyValPheAlaAlaGlyAspValGlnAspLysLysTyArgGlnAlaIleThr 304
Db 1227094 GTGGAAGCGGTGTTTCGACAGCGCATGTCTATGATACCAATTCGCAAGCCATTACC 1227035
QY 305 AlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyLeu 320
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Search completed: June 21, 2004, 20:53:06
Job time : 3376 secs

QY 601 AGGGGCTCTCAATCCTAAGATCCAGGTTCTTGGGACTCGAGGTGCTGAGGCTTACG 660
DB 601 AGGGGCTCTCAATCCTAAGATCCAGGTTCTTGGGACTCGAGGTGCTGAGGCTTACG 660
QY 661 GGGGTGAGGGGGGGGGCCATTAGTGGGGTCAAGGTCAAGAACTTGGTGAAGTGGTGAAG 720
DB 661 GGGGTGAGGGGGGGGGCCATTAGTGGGGTCAAGGTCAAGAACTTGGTGAAGTGGTGAAG 720
QY 721 TGCTGAAGTTCAGGTGCTGGGGTCTTTCGGCATCGGGCATGAGCCGGCCACCAAGT 780
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DB 781 TTCTCAATGGGAGGCTTCAGGCTCCATGCGGATGGGTATGTGCGCACCAAGCCGGGCTCTA 840
QY 841 CACATACCAGTGTGAGGGGCTTTTGGCTGGAGAGCTGAGGATGAAGAGTATCGTCA 900
DB 841 CACATACCAGTGTGAGGGGCTTTTGGCTGGAGAGCTGAGGATGAAGAGTATCGTCA 900
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DB 901 GGCCATTACTGCTGGATCAGGTTGATGCTGCTGGAGAGCTGAGGAGCGCGAGCACTATCTGC 960
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DB 961 AGGAGGTGGGTGCACAGGTGGGCAAGTCTGATTGA 995

RESULT 3

US-10-425-114-5073
; Sequence 5073, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 5073
; LENGTH: 1286
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700447274_FLI
US-10-425-114-5073

Query Match 74.2%; Score 738.6; DB 13; Length 1286;
Best Local Similarity 85.8%; Pred No. 3.2e-180;
Matches 855; Conservative 0; Mismatches 139; Indels 3; Gaps 3;
QY 1 ATGAGGGATCCGCGCGCGCGCTCCGCGCGCGGTGCGATCATCGGAGCGGCCG 60
DB 58 ATGAGGGATCCGCGCGCGCGCTCCGCGCGCGGTGCGATCATCGGAGCGGCCG 117
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DB 118 GTGCGCACACGCGCGCGCTTACGCGCGCGCGCGGAGCTCAAGCCGCTCTTCGAG 177
QY 121 GGTGATGGCAACGACATCCGCGCGCGCGCGCGAGCTCACCACCAACCGAGTCGAG 180
DB 178 GGTGATGGCAACGACATCCGCGCGCGCGCGAGCTCACCACCAACCGAGTCGAG 237
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DB 238 AACTTCCCGGATTCGCCACCGGATCATGGGCGCGCGCTCATGACACTGCGCGCG 297

QY 241 CAGTCCGTCCGTTCCGCGCGCGCGCTTCTCTCGAGACCGTCAACGAGTCCGACTTCTCC 300
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DB 358 GCTTCCCATTTCCGAGTTAGTGAAGTCCCAACCGTCTCCGCGATCGGTTATCGTT 417
QY 361 GCCACGGGCGCGTCCGCGCGCGCTTCTCCATTTCTCCGTTCCGACACCTTATGGAACCGC 420
DB 418 GCCACGGGCGCGTCCGCGCGCGCTTCTCCATTTCTCCGCGGTCCGATGATCTGGAACCGC 477
QY 421 GGCATCTCCGCTCCGCGTCCGCGTCCGCGCGCGTCCGCGCGCTTCTCCGCGACAGCGCCATC 480
DB 478 GGCATCTCCGCTCCGCGTCCGCGTCCGCGCGCGTCCGCGCGCTTCTCCGCGACAGCGCCATC 537
QY 481 GCGGTATCCGCGCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCCGCG 540
DB 538 GCGGTATCCGCGCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCCGCG 597
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DB 718 GCGCGCGCAACCGCGCGCGCTTATAGTGGGGTCAAGGTCAAGAACTTGGTGAAGTGGTGAAG 777
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DB 778 GTCTCTGACCTTCAGGTGCTCCGCGCTTCTTCGCGCATCGGCGTCCGCGCGCGCGCGCGCG 837
QY 780 TTTCTCAATGGGCGCGTTCAGTCCATGCGATGGGTATGTGGCGCGCGCGCGCGCGCGCTCT 839
DB 838 TTTCTGGGCGCGCGCGCTTGAACCTCGATTCAGATGGTTATGCGAAACCAAGCGCGCGCTTC 897
QY 840 ACACATACAGTGTGAGGGG-GTCTTTTGTCTGGGAGAGTGCAGATGAAGAGTATCGT 898
DB 898 ACTCACACAGTGTAAAGGTTGTTTCTGCTGGCGAGCTGCGAGCAAGAGTATCGT 957
QY 899 CAGGCGCATTTACTGCTGCTGATCGAGTTCAGTGGCTGCTTTGGGAGCGCGGAGCACTATCT 958
DB 958 CAGGCGCATTTACTGCTGCTGATCGAGTTCAGTGGCTGCTTTGGGAGCGCGGAGCACTATCT 1016
QY 959 GCAGGAGTGGGTGCACAGGTGGGCGAAGTCTGATTGA 995
DB 1017 GCAGGAGTGGGTGCACAGGTGGGCGAAGTCTGATTGA 1053

RESULT 4

US-10-425-114-3716
; Sequence 3716, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCES: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 3716
; LENGTH: 1325

TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700336177_FLI
US-10-425-114-3716

Query Match 74.2%; Score 738.6; DB 13; Length 1325;
Best Local Similarity 85.8%; Pred. No. 3.2e-180;
Matches 855; Conservative 0; Mismatches 139; Indels 3; Gaps 3;

QY 1 ATGAGGATCCCGCGCGCGCTCCGACGCGGTGTCATCGGACGCGCGCG 60
DB 87 ATGAGGATCCCGCGCGCGCTCCGCTCCGACGCGCATCTGATCATCGGAGCGGTCCC 146
QY 61 GCGCGCACACGCGCGCATCTACGCGCGCGCGCGGAGCTCAAGCCCGTCTTTCGAG 120
DB 147 GCTGGCACACGCGCGCATCTACGCGCGCGCGCGGAGCTCAAGCTGTCTTCGAG 206
QY 121 GGTGGATGGCAACACATCGCGCGCGCGCGGAGCTCAACACACGCGCGCGTTCGAG 180
DB 207 GGTGGATGGCAACACATCGCGCGCGCGCGGAGCTCAACACACGCGCGCGTTCGAG 266
QY 181 AACTTCCCGGATTCGCCACGCGCATCGGCGCATCGGCGCATCGGCGCATCGGCGCG 240
DB 267 AACTTCCCGGATTCGCCACGCGCATCGGCGCATCGGCGCATCGGCGCATCGGCGCG 326
QY 241 CAGTCGCTCGGCTTGGCGACCAATCTCTCGGACGCGTCAACGAGTCACTTCTCC 300
DB 327 CAGTCGCTCGGCTTGGCGACCAATCTCTCGGACGCGTCAACGAGTCACTTCTCC 386
QY 301 GCGCGCGCTTCGCGCGTCACTCGGACTCCACACGCTCTCGGCGCACGCGTCTGCG 360
DB 387 GCTTCCCGATTCGAGTAGTGAGACTCAACACGCTCTCGGCGCATCGGCTTTCGTT 446
QY 361 GCGACGCGCGCTTCGCGCGCGCTCTCAATTTCTCGGTTTCGACACTTCTGGAACGCG 420
DB 447 GCGACGCGCGCTTCGCGCGCGCTCTCAATTTCTCGGTTTCGACACTTCTGGAACGCG 506
QY 421 GGCATCTCCGCTTCGCGCGCTTCGCGCGCGCTTCGCGCGCATCTTCGCGACGCGCATC 480
DB 507 GGCATCTCCGCTTCGCGCGCTTCGCGCGCGCTTCGCGCGCATCTTCGCGACGCGCATC 566
QY 481 GCGGTCTATCGCGCGCGTGTATTCGCGCATCGGAGGAGCAACTTCTCAACGATACGGA 540
DB 567 GCGGTCTATCGCGCGCGTGTATTCGCGCATCGGAGGAGTCCAAATTTCTCAACGATACG 626
QY 541 TCCCAAGTGTACATCTCCGCGCGCGTTCGCGCGCGTTCGCGCGCATCTTCGCGACGCGCATC 600
DB 627 TCCCAAGTGTACATCTCCGCGCGCGTTCGCGCGCGTTCGCGCGCATCTTCGCGACGCGCATC 686
QY 601 AGGCGGCTCTCCAAATCTTAAGATCCAGGTTGTCTGGGACTC-GAGGTCTGTCGAGGCTTAC 659
DB 687 AGGCGGCTCTGAACACCCAAATTAAGTCTCTGGGACTCGGAAGTTGTGAGGCTTAT 746
QY 660 GCGCGTCAAGCGCGCGCGTTCGCGCGCGTTCGCGCGCGTTCGCGCGCATCTTCGCGACGCGCATC 719
DB 747 GCGCGTCAAGCGCGCGCGTTCGCGCGCGTTCGCGCGCGTTCGCGCGCATCTTCGCGACGCGCATC 806
QY 720 GTGTCTGACCTTCAAGTGTCTGGGCTTTCTTTCGCGCATCGGCGCATCGGCGCGCATCAAG 779
DB 807 GTGTCTGACCTTCAAGTGTCTGGGCTTTCTTTCGCGCATCGGCGCATCGGCGCGCATCAAG 866
QY 780 TTTCTCAATGGGCGAGTTCGCGCGTTCGCGCGCGTTCGCGCGCATCGGCGCGCATCAAGCGGCTCT 839
DB 867 TTTCTGGGCGGACAGTTCGCGCGTTCGCGCGCGTTCGCGCGCATCGGCGCGCATCAAGCGGCTCT 926
QY 840 ACACATACCACTGTGGAGGG-GTCTTTGCTGTGGAGCGTTCGCGCGCATCGGCGCGCATCAAGCGGCTCT 898
DB 927 ACTCACACCACTGTAAAGGTTGATTTGCTGTGGAGCGTTCGCGCGCATCGGCGCGCATCAAGCGGCTCT 986
QY 899 CAGGCGCAATCTGCTGTGGATCAGGTTGATGCTCTTGGGACGCGCGCATCTATCT 958
DB 987 CAGGCGCAATCTGCTGTGGATCAGGTTGATGCTCTTGGGACGCGCGCATCTATCT 1045

QY 959 GCAGGAGGTGGTGCACAGGTGGGCAAGTCTGATTGA 995
DB 1046 GCAGGAGGTGGTGCACAGGTGGGCAAGTCTGATTGA 1082

RESULT 5

US-10-306-292-26
Sequence 26, Application US/10306292
Publication No. US20030145347A1
GENERAL INFORMATION:
APPLICANT: Lanahan, Michael B.
APPLICANT: Desai, Nalini M.
APPLICANT: Gaudaska, Pamela Y.
TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
FILE REFERENCE: A-31383PI
CURRENT APPLICATION NUMBER: US/10/306,292
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: US/09/598,747
PRIOR FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 1560
TYPE: DNA
ORGANISM: Oryza sativa
US-10-306-292-26

Query Match 74.1%; Score 737.6; DB 15; Length 1560;
Best Local Similarity 88.6%; Pred. No. 5.9e-180;
Matches 822; Conservative 0; Mismatches 104; Indels 2; Gaps 2;

QY 1 ATGAGGAGTCCGCGCGCGCTCCGACGCGGTGTCATCGGACGCGCGCGCG 60
DB 406 ATGAGGAGTCCGCGCGCGCTCCGACGCGGTGTCATCGGAGCGGCGCG 465
QY 61 GCGCGCACACGCGCGCGCATCTACGCGCGCGCGCGGAGCTCAAGCCCGTCTTCGAG 120
DB 466 TCGGCGCACACGCGCGCGCATCTACGCGCGCGCGCGGAGCTCAAGCCCGTCTTCGAG 525
QY 121 GGTGGATGGCAACACATCGCGCGCGCGCGGAGCTCAACACACGCGCGTTCGAG 180
DB 526 GGTGGATGGCAACACATCGCGCGCGCGCGGAGCTCAACACACGCGCGTTCGAG 585
QY 181 AACTTCCCGGATTCGCCACGCGCATCGGCGCATCGGCGCATCGGCGCATCGGCGCG 240
DB 586 AACTTCCCGGATTCGCCACGCGCATCGGCGCATCGGCGCATCGGCGCATCGGCGCG 645
QY 241 CAGTCGCTCGGCTTGGCGACCAATCTTCGAGACGCGTCAACGAGGTCGATCTTCC 300
DB 646 CAGTCGCTCGGCTTGGCGACCAATCTTCGAGACGCGTCAACGAGGTCGATCTTCC 705
QY 301 GCGCGCGCTTCGCGCGTTCGCGCGTTCGCGCGTTCGCGCGCATCTTCGCGACGCGCATC 360
DB 706 GCGCGCGCTTCGCGCGTTCGCGCGTTCGCGCGTTCGCGCGCATCTTCGCGACGCGCATC 765
QY 361 GCGCGCGCGCTTCGCGCGTTCGCGCGTTCGCGCGTTCGCGCGCATCTTCGAGAACGCG 420
DB 766 GCGCGCGCGCTTCGCGCGTTCGCGCGTTCGCGCGTTCGCGCGCATCTTCGAGAACGCG 825
QY 421 GGCATCTCCGCGTTCGCGCGTTCGCGCGTTCGCGCGTTCGCGCGCATCTTCGAGAACGCGCATC 480
DB 826 GGCATCTCCGCGTTCGCGCGTTCGCGCGTTCGCGCGTTCGCGCGCATCTTCGAGAACGCGCATC 885
QY 481 GCGGTCTATCGGCGCGGTGATTCCGCGCATCGGAGGAGCAACTTCTTCACCAAGTACGGA 540
DB 886 GCGGTCTATCGGCGCGGTGATTCCGCGCATCGGAGGAGTCCAAATTTCTTCACCAAGTACG 945
QY 541 TCCCAAGTGTACATCTCAACGCGCGGAGCAACTTTCGCGCGCTTCGAGTATTCGAGCT 600
DB 946 TCCCAAGTGTACATCTCAACGCGCGGAGCAACTTTCGCGCGCTTCGAGTATTCGAGCT 1005

Query Match	53.2%	Score 529	DB 13	Length 1284
Best Local Similarity	75.1%	Fred. No. 2.5e-126		
Matches 732	Conservative 0	Mismatches 225	Indels 18	Gaps 5
Qy	38	TGTGCATCATGGCAGCGCCGCGCGCACAGCGGGCCATCTACGGCGCGCGCGG	97	
Db	64	TCTGCATCATCGAAGCGGTCCCTCCGCGCCACACAGCGCGGTCTACGCGCTCAGCGCG	123	
Qy	98	AGCTCAAGCCGGTCTCTTCAGAGGCTGGATGGCCAAAGCATCGCGCGGGGGGCGCAGC	157	
Db	124	AGCTGAAGCCGATCCTCTTCAGAGGCTGGATGGCCAAAGCATCGCGCGGGGGGCGCAGC	183	
Qy	158	TCACCAACCAACCGAGCGTCGAGAACTTCCCGGATTCGCCACCGGCATCATGGGCATCG	217	
Db	184	TCACCAACCAACCGAGCGTCGAGAACTTCCCGGATTCGCCACCGGCATCATCGCGCGCG	243	
Qy	218	ACTCATGAGCAACTGCGGGCGCCAGTCGCTCGCTTCGGACCAACATCCTCTCCGAGA	277	
Db	244	AGCTCATGAGCAACTGCGGGCGCCAGTCGCTCGCTTCGGACCAAGATCCACACCGAGA	303	
Qy	278	CCGTCACCGAGGTGCACTTCTCCGCCCGCCCTTCGCGTCACCTCCGACTCCACCAACCG	337	
Db	304	CCGTCCTCAAGTCGATTTCTCGAAACCGTCTTTTCAGGGTTTTTTCACCGATTCGCCGAACCG	363	
Qy	338	TCCTTCGCGGACACGTCGTCGCGCACGGGCGCGCTCGCGCGCGGCTCCATTTCTCCG	397	
Db	364	TGAGGCCGAATCCGTCATGTCGCGCACGGTGCCTGCGCAAGCGCTTCCCTTTCGCCG	423	
Qy	398	GT-----CCGACACCTTACTGGAACCGCGCATCTCCGCTCGGCGCTGCTGCG	445	
Db	424	GCTCCGCGGACGCGCCCGAAGGCTACTTGGAAACCGTGGAACTCTCCGCTGCGCGCTGCG	483	
Qy	446	ACGCGCTGCGCCCATCTTCGGGAACAGCCCATCGCGCTCATCGCGGGGGTGATTCG	505	
Db	484	ACGCGCGCGCCCGATCTTCGGGAACAGCCCGTGGCAGTGATCGCGGGGGGAGACTCCG	543	
Qy	506	CCATGGAAGGCAACTTCTCAACCAAGTACCGATCCCAAGTGATCATCATCCACGGCG	565	
Db	544	CCATGGAAGGCAACCTTCTCAACCAAGTACCGATCCCAAGTTTTCGAATTCACCGTA	603	
Qy	566	GCACACTTCCGCGCTCCAGATTATGCAAGCTAGGGGCTCTCCCAATCCTAAGATCC	625	
Db	604	GGGATAGTTTCAGGGCTTCGAAGATTATGCAAGCAAGGTGATGAATATAGTAGAATTA	663	
Qy	626	AGGTGTCTGGACTC-GAGTCTCGAGGCTTACCGCGGTGACGGGGCGGGCCCATAG	684	
Db	664	AGGTGATTTGGAATTCGGTGTGGTGTTCAGGCTTTTGGGGCGGAGATAACAAGAGGTGC	723	
Qy	685	CTGGG---TCAGGTCAAGNACTTGCTGACTGTGTGAGGTGTCTGACCTTCAGGTGTCG	741	
Db	724	TTGGGGGATGGAAGGTGAAGAAATGTGTGACTCAAGAGGTGTCTGAATTAAGAGTTTCTG	783	
Qy	742	GGCTTTTCTTCGCCATCGGGGCACTAGCGCGGCACCAAGTTTCTCAATGGGCGAGCTTGAGC	801	
Db	784	GGTTGTTTTTCGCAATTTGGGCACGAGCCCGGACCAAGTTCTTGGACGGGCGAGCTTGAAT	843	
Qy	802	TCCATGCGGATGGGTATGTGGCACCAAGCGGGCTCTACACATACAGGTGTGAGGG-G	860	
Db	844	TGGATTTCTGATGGGATATATTGTGACGAAGCGGGGACGAGGAACCAAGTGTGAGGGAG	903	
Qy	861	TCTTTGCTGCTGGAGACGTGCAGGATAGAAGTATCGTCAAGGCCATTTACTGCTCTGGAT	920	
Db	904	TGTTTGCTGCTGGGATGTTTCAGGACAAAGTATAGCAAGCTATTACTGCTGCTGCA	963	
Qy	921	CAGGTCGATGGCTGCTTTTGGACGCGCGGACACTATCTGAGGAGGTGGGTGACAGGTG	980	
Db	964	CTGATGCACTGGCTGCTTTT-GGATGCAAGCAATTACCTGCAAAATGTGTGTTTCAACAA	1022	
Qy	981	GGCAAGTCTGATGA 995		
Db	1023	GATAAGAGTGATTGA 1037		

```

RESULT 8
US-10-424-599-65583
  ? Sequence 65583, Application US/10424599
  ? Publication No. US20040031072A1
  ? GENERAL INFORMATION:
  ? APPLICANT: La Rosa Thomas J
  ? APPLICANT: Kovalic David K
  ? APPLICANT: Zhou Yihua
  ? APPLICANT: Cao Yongwei
  ? TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
  ? TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
  ? FILE REFERENCE: 38-21(63223)B
  ? CURRENT APPLICATION NUMBER: US/10/424,599
  ? CURRENT FILING DATE: 2003-04-28
  ? NUMBER OF SEQ ID NOS: 285684
  ? SEQ ID NO 65583
  ? LENGTH: 1645
  ? TYPE: DNA
  ? ORGANISM: Glycine max
  ? FEATURE:
  ? OTHER INFORMATION: Clone ID: PAT_MRT3847_30236C.1
US-10-424-599-65583

```

Query Match	52.7%	Score 524.2	DB 13	Length 1645
Best Local Similarity	74.8%	Pred. No. 4.4e-125		
Matches 729	Conservative 0	Mismatches 228	Indels 18	Gaps 5
QY	38	TGTGATCATCGGACGGCCGCGCACACGGCGGCATCTACGGCGCCCGCGG 97		
Db	176	TCTGATCATTGGAAAGCGTCCCTCCGCCACACAGCGCGCTCTACGGCTCGAGCGC 235		
QY	98	AGCTCAAGCCCGTGCTCTTTCGAGGGCTGGATGSCCAACGACATCGCCGGGGGGCCACG 157		
Db	236	AGCTGAAGCCGATCTCTTTCGAGGGCTGGATGSCCAACGACATCGCCCGCGCGCCACG 295		
QY	158	TCACACACACACGAGCTCGAGAACTTCCCGGATTCGCCACCGCGCATCTAGGGCATCG 217		
Db	296	TACACACACACGAGCTCGAGAACTTCCCGGGTTCCCGACGGCATCTCTCGGGGGGG 355		
QY	218	ACCTCATGACAACTGCGCGCCCGACGCTCCGCTTCGGCACCAACATCTCTCCGAGA 277		
Db	356	AGCTCATGGAAGCTGCGGAGCCAGTCGCTCCGCTTCGGCACCGAGATCCACACCGAGA 415		
QY	278	CGGTACACGAGTGACATTCTCCGCGCCGCCCTTTCGCGCTGACCTCCGACTCACACCGC 337		
Db	416	CGGTCTCCAAAGTCGATTCTTCGAACCGCTCTTTCAGGGGTTTTTCACCGATTCGCCAACCG 475		
QY	338	TCTCTCGCGACACCGTCTGTCTGCCACGAGCGCGCTTCGGCGCGCGCTCCATTCTCCG 397		
Db	476	TGAGGCGGATTCGTCATGCTGCCACCGCGCGCTTCGCCAAGCGCTCCCGCTCCCGC 535		
QY	398	GT-----CGACACCTACTGGAACCGCGCATCTCCGCTTCGCGCTGTGCG 445		
Db	536	GCTCCGCGATGCGCCCGATGGCTACTTGAACCGCGCATCTCCGCTTCGCGCTGTGCG 595		
QY	446	ACGGCGCTCGCCCATCTTTCGGACACAGCCCATTCGCGCTCATCGCGGGGGTGATTCCG 505		
Db	596	ATGGCGCGCGCCCATCTTTCGGAAACAAAGCCACTTCGGCGGTGATTCGGCGCGGGGACTCG 655		
QY	506	CCATGAGGAGAGGCAATCTCTCACCAGTACGGATCCCAAGTGATCATCTCCACCGCGC 565		
Db	656	CGATGAGGAGGCCACCTTCTCACCAGTACGGTTCGAGGTTTACATAATTCACCGCA 715		
QY	566	GCAACACCTTCGGCGCTCCAAAGTATGACGGGTAGGGGCTCTCCATTCCTAGATGCC 625		
Db	716	GGGATACATTGAGGCTTCGAAGATTATGCAGACGCAAGGTTATGGGCAATAGCAAGATTA 775		
QY	626	AGGTTGCTCGGACTC-GAGTCTGTGAGGCTTACGGCGGTGCAGGCGCGGCCCATTAG 684		
Db	776	AGGTGATTTGAAATTTCGGTGGTTCGAGGCTTTGGGGCGGAGTAAACAGAGGGTGC 835		
QY	685	CTGGGG-----TCAAGTCAAGAACTTGGTGACTCGTGAGGTGTCTGACCTTCAGGTGTCCG 741		

Db 836 TTGGGGATTGAAGGTGAAGAAATGTGTGACTCGAGAGTATCTGAATTAAGGTTTCTG 895
Qy 742 GGCTTTTCTTCGGCCATCGGCGATGAGCGCGCCACCAAGTTTCTCAATGGCGAGCTTGAGC 801
Db 896 GGTGTGTTTTCGCAATTGGSCACGAGCCCGGACCAAGTTCTTGGACGGCGAGCTTGAAT 955
Qy 802 TCATCGCGATGGGTATGTGGCCACCAAGCGCGGCTCTACACATACAGTGTGGAGG-G 860
Db 956 TGAATTTCTGATGATATATTGTGACGAAGCGCGGACGACGAGACAGTGTGTGAGGGAG 1015
Qy 861 TCTTTGCTGCTGAGAGCTGACGATGAAGATATCGTCAGGGCAATTACTGTCTGCTGGAT 920
Db 1016 TGTGTTGCTGCTGGGATGTTTCAGCAACAGAGTATAGGCAAGTATTAATGCTGCTGCA 1075
Qy 921 CAGGTTGATGCTGCTTTGGGACCGCGACATATCTGACGAGGTGGTGACAGGTG 980
Db 1076 CTGATGATGCTGCTGCTTT-GGATGACAGACATTAATCTGCAAAATGTTGTTTACACAA 1134
Qy 981 GGCAAGTCTGATTGA 995
Db 1135 GATAAGAGTGAATTGA 1149

RESULT 9
US-10-424-599-13171
; Sequence 13171, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 13171
; LENGTH: 964
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_1118C.1
US-10-424-599-13171

Query Match 47.9%; Score 476.8; DB 13; Length 964;
Best Local Similarity 71.6%; Pred. No. 6.6e-113;
Matches 686; Conservative 0; Mismatches 257; Indels 15; Gaps 4;

Qy 28 CGCAGCGCGTGTGCATCATCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 87
Db 7 CGTCCGAAGCTCTGCATCATCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 66
Qy 88 GCCCGCGCGGCTCAAGCGCGTCTTTCGAGGCTGGATGGCCACGACATCGCGCG 147
Db 67 CGCGCGCGCGAGTTGAAGCGCGTCTTTCGAGGCTGGATGGCCACGAGCGCGTCTCC 126
Qy 148 GGGGGCCAGCTCACACACACCGAGCTCGAGAACTTCCCGGATTCGCCACCGGCATC 207
Db 127 GGTGGCCAGCTCACACACACCGAGCTCGAGAACTTCCCGGATTCGCCCGCGGCATC 186
Qy 208 ATGGGATGACCTCATGAGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 267
Db 187 CTGGGACCGAGCTCATGAGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 246
Qy 268 CTCTCCGAGACCGTCAAGCGAGTGCATCTTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 327
Db 247 GTACGAGGACCGTCAAGCGAGTGCATCTTCTCCGAGCTTCTCCGAGTTCGAGTTCGAGC 306
Qy 328 TCACACACCGTCTCGCGGACACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 387
Db 307 TCACACACCGT 366

RESULT 10

US-10-290-072-38
; Sequence 38, Application US/10290072
; Publication No. US20030211511A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Daimia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Lugimbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-3
; CURRENT APPLICATION NUMBER: US/10/290,072
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/376,682
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 10/141,531
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 6357
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-290-072-38

Query Match 43.0%; Score 427.4; DB 13; Length 6357;
Best Local Similarity 67.5%; Pred. No. 3.9e-100;
Matches 666; Conservative 0; Mismatches 306; Indels 15; Gaps 4;

QY 23 CGTTCGCGACGGCGGTGTCATCGGCGAGCGCGCGCGCGCGCACACGCGCGCATCT 82
DB 5350 CTCACACACAGGCTCTGTATCGTAGGAGTGGCCAGCGCACACACGCGCGCATTT 5409

QY 83 ACGCGCGCGCGCGGAGCTCAAGCGCGTCTTCGAGGCTGGATGGCCACAGCATCG 142
DB 5410 ACGCGAGCTAGGCTGAACCTTCTCTCGAAGGATGGATGCTAACGACATCG 5469

QY 143 CCGCGGGGGCGAGCTCACACACACGAGCTCGAGAACTTCCCGGATTCGCCACCG 202
DB 5470 CTCGCCGTGCTCACTAAACACACACGAGCTGAGAACTTCCCGGATTCAGAG 5529

QY 203 GCATCATGGGATTCGACCTCACTGAGCAACTGCGCGCGCGAGTCCGCTTCGCGACCA 262
DB 5530 GTATTCTCGGAGTAGAGCTCACTGACAAATTCGGTAAACAAATCGGAGGATTCGGTACTA 5589

QY 263 ACATCTCTCCGAGACCGTCAAGGCTGAGTCTTCTCGCGCGCGCTTCGCGTCACT 322
DB 5590 CGATATTCAGAGACGCTGAGAACTGCTTCTTCGAAACCGTTTAAGCTATTCA 5649

QY 323 CCGACTCCACACCGTCTCGCGACACGCTCGTTCGCGCGCGCGCGCGCGCGCGCG 382
DB 5650 CAGATTCCAAAGGCACTTCTCGCTGACGCTGATTTCTGCTACTGAGCTGTGGCTAAGC 5709

QY 383 GCTCCATTC-----TCCGTTCCGACACCTACTGGAACCGCGCATCTCG 430
DB 5710 GGTATTAGTCTGTTGATCTGTTGAGGTTCTGAGGTTCTGGAACCGTGAATCTCG 5769

QY 431 CTGCGCGCTCTCGACGCGCTCGCGCATCTTCGGAACAAAGCCCATCGCGTCACTCG 490
DB 5770 CATGCGCTGTTTCGACGCGAGCTGCTCGATATTCGTTAAACAACTCTTCGGGTGATCG 5829

QY 491 GCGCGGTTATTCGCGATCGAGGAGCACTTCTCACCAAGTACGATCCGAGTGT 550
DB 5830 GTGAGGCGATTTCAGCAATGGAAGAGCAAACTTCTTACAAATATGATTCGAAAGTGT 5889

QY 551 ACATCATCCACGCGCGCAACACCTTCGCGCGCTTCCAAAGATTATGAGGCTAGGCGCTCT 610
DB 5890 ATATAATCCATCGCGCGATGCTTTTCGTTGCTTAAAGATTATGAGCGCGCTTTGT 5949

QY 611 CCAATCTTAAGTCCAGGTTGTTCGGAATCG-AGTCTCGAGGCTTAAGCGGTGCGAG 669
DB 5950 CTAATCTTAAGATTGATGATTTGGAATCTGCTGTTTGTGGAAGCTTATGAGATGGAG 6009

QY 670 GCGCGCGCGCATTAGCTGGGCTCAAGCTCAAGAACTTGGTGAAGTCTGAGGCTCTGACC 729
DB 6010 AAAGAGATGCTTGGAGGATTGAAGTGAAGATGCTGTTACCGGTGATGTTCTGATT 6069

QY 730 TTCAAGTGTCCGGGCTTTTCTTCGCCATCGCGGATGAGCGCGCGCACCAAGTTTCTCAATG 789
DB 6070 TAAAGTTTCTGGAATGTTCTTTGCTATTGTTGATGAGCCAGCTACCAAGTTTTCGATG 6129

QY 790 GGCAGCTGAGCTCCATCGGATGGGTATGTCGACCAAGCGCGGCTCTACACATACCA 849
DB 6130 GTGGTGTGAGTTAGATTGGATGGTTATGTTGTACAGAGGCTGTGACTACACAGCTA 6189

QY 850 GTG-TGAGGGGTCTTTGCTGTGAGAGAGCGTGAAGATTAAGATATGTCAGGCCATTA 908
DB 6190 GCGTTCCCGGAGTTTTCGCTGCGGGTGATGTTTTCAGGATTAAGATATAGGCAAGCCATCA 6249

QY 909 CTGCTGCTGATCAGGTTGATGCTGCTTTCGGAAGCGCGGACCTATCTGCAAGAGGTG 968
DB 6250 CTGCTGAGAACTGGGTGCAATGGCAAGCTTTTGGATGCAAGCACTTATTCACAGAGATT 6308

QY 969 GGTGCAAGGTGGCGAAGTCTGATTCA 995
DB 6309 GGATCTCAGCAAGGTAAGAGTATGCA 6335

RESULT 11
US-10-141-531-38
; Sequence 38, Application US/10141531
; Publication No. US20030100743A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Luginbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioresdoxin Reductase Activity
; FILE REFERENCE: A-71457-2/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/141,531
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 6357
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-141-531-38

Query Match 43.0%; Score 427.4; DB 15; Length 6357;
Best Local Similarity 67.5%; Pred. No. 3.9e-100;
Matches 666; Conservative 0; Mismatches 306; Indels 15; Gaps 4;

QY 23 CGTTCGCGACGCGGTGTCATCGGCGAGCGCGCGCGCGCGCACACGCGCGCATCT 82
DB 5350 CTCACACACAGGCTCTGTATCGTAGGAGTGGCCAGCGCACACACGCGCGCATTT 5409

QY 83 ACGCGCGCGCGGAGCTCAAGCGCGTCTTCGAGGCTGGATGGCCACAGCATCG 142
DB 5410 ACGCGAGCTAGGCTGAACCTTCTCTTCGAGGATGGATGGCTTAAAGCATCG 5469

QY 143 CCGCGGGGGCGAGCTCACACACACGAGCTCGAGAACTTCCCGGATTCGCCACCG 202
DB 5470 CTCGCCGTGCTCACTAAACACACACGAGCTGAGAACTTCCCGGATTCAGAG 5529

QY 203 GCATCATGGGATTCGACCTCACTGAGCAACTGCGCGCGCGAGTCCGCTTCGCGACCA 262
DB 5530 GTATTCTCGGAGTAGAGCTCACTGACAAATTCGTTAAACAAATCGGAGCGATTGGTACTA 5589

QY 263 ACATCTCTCGAGACCGTCAAGGCTGAGTCTTCTCGCGCGCGCTTCGCGTCACT 322
DB 5590 CGATATTCAGAGACGCTGAGAACTGCTTCTTCGAAACCGTTTAAGCTATTCA 5649

QY 323 CCGACTCCACACCGTCTCGCGACACGCTCGTTCGCGCGCGCGCGCGCGCGCGCG 382
DB 5650 CAGATTCCAAAGGCACTTCTCGCTGACGCTGATTTCTGCTACTGAGGCTGTGGCTAAGC 5709

QY 383 GCTCCATTC-----TCCGTTCCGACACCTACTGGAACCGCGCATCTCG 430
DB 5710 GGTATTAGTCTGTTGATCTGTTGAGGTTCTGAGGTTCTGGAACCGTGAATCTCG 5769

QY 431 CTGCGCGCTCTCGACGCGCTCGCGCATCTTCGGAACAAAGCCCATCGCGTCACTCG 490
DB 5770 CATGCGCTGTTTCGACGCGAGCTGCTCGATATTCGTTAAACAACTCTTCGGGTGATCG 5829

QY 491 GCGCGGTTATTCGCGATCGAGGAGCACTTCTCACCAAGTACGATCCGAGTGT 550
DB 5830 GTGAGGCGATTTCAGCAATGGAAGAGCAAACTTCTTACAAATATGATTCGAAAGTGT 5889

QY 551 ACATCATCCACGCGCGCAACACCTTCGCGCGCTTCCAAAGATTATGAGGCTAGGCGCTCT 610
DB 5890 ATATAATCCATCGCGCGATGCTTTTCGTTGCTTAAAGATTATGAGCGCGCTTTGT 5949

611	Qy	CCAAATCCTTAAGATCCAGAGTTGTCTGGGACATCG-AGTCTGTCGAGGCTTACGGCGGTGCAG	669
5950	Db	CTAATCCTAAGATTGATGATTGGAACTCGTCTGTGTGGAAGCTTATGAGAGTCGAG	6009
670	Qy	GCGCGGCCCCATTAGCTGGGGTCAAGGTCAAGAACTTGGTGACTGGTGAAGGTCTCTGACC	729
6010	Db	AAAGAGATGTCTTGGAGGATTGAAGTGAAGAAATGTGGTTACCGGTGATGTTTCTGATT	6069
730	Qy	TTCAAGTGTCCGGGCTTTTCTGCCCATCGGCATGAGCCGGCCACCAGAGTTTCTCAATG	789
6070	Db	TAAAGTTTCTGGATTGTTCTTGTCTATTGTCATGAGCCAGCTACCAAGTTTGGATG	6129
790	Qy	GGCAGCTTGAGTCCATCGCCGATGGGTATGTGGCCACCAAGCCGGGCTCTACACATACCA	849
6130	Db	GTGGTGTGTAGTTAGATTTCGGATGGTTATGTTGTCTACGAAGCCCTGGTACTACACAGACTA	6189
850	Qy	GTG-TGAGAGGGTCTTTGTCTCTGGACACTGCGAGGATAGAAGTATCGTCAGGCCATT	908
6190	Db	CGGTTCCCGAGTTTTCGTCGGGGTATGTTTACGGATAGAAGTATAGGCAAGCCATCA	6249
909	Qy	CTGTGCTGGATCAGGTTTGCATGCTCTTTTGGACGCCGAGCACTATCTGCGAGGAGTG	968
6250	Db	CTGCTCGAGGACATGGGTGCATGCGACGTTT-GGATCGAGGCATTACTTACAAGAGATT	6308
969	Qy	GGTGCA CAGGTGGGCAAGTCTGATTGA	995
6309	Db	GGATCTCAGCAAGGTAAGTGTATGGA	6335

RESULT 12

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US-10-290-072-40
; Sequence 40, Application US/10290072
; Publication No. US2003021151A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Helfetz, Peter
; APPLICANT: Luginduhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioresodoxin Reductase Activity
; FILE REFERENCE: A-71457-3
; CURRENT APPLICATION NUMBER: US/10/290,072
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/376,682
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 10/141,531
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 6357
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-290-072-40

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RESULT 13
US-10-290-072-42
; Sequence 42, Application US/102900072
; Publication No. US/003021151A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: Dalmia, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Helfetz, Peter

5410	Db	ACGAGCTAGGGCTGAACCTTAAACCTCTCTCTCGAAGGATGGATGGCTAACGACATCG	5469
143	QY	CGCGGGGGCGAGCTCAACCAACCAACGAGCTCGAGAACTTCCCGGATTCGCCACCG	202
5470	Db	CTCCCGGTGGTCAAATAACCAACCAACGAGCTCGAGAAATTCGCCGATTTCCAGAAAG	5529
203	QY	GCATCATGGGCATCGACCTCATGGACAACTCGCGCGCCCGAGTCCGTCCTTCGGCACCA	262
5530	Db	GTATTCTCGGATAGAGCTCACTGACAAATTCGGTAAACATCGGAGCGATTCGGTACTTA	5589
263	QY	ACATCCTCTCCGAGACCGTCAACGAGGTGCACTTCTCCGCCCGCCCTTCCGCGTCACCT	322
5590	Db	CGATATTTACAGAGCGGTGACGAAAGTCGATTTCTCTCGAAAACGTTTAAAGCTATTCA	5649
323	QY	CCGACTCCACACCGTCTCCGCCGACACCGTGGTGGCCACGGCGCGCGTCCGCGCC	382
5650	Db	CAGATTCCAAAGCCATTCTCGCTGACGTGTGATTTCTCGCTACTGGAGCTGTGGCTAAGC	5709
383	QY	GCCTCCATTTC-----TCGGTTCGGACACCTACTGGAAACCGCGGCATCTCCG	430
5710	Db	GGCTTAGCTTCGTTGGATCTGGTGAAGGTTCTGGAGGTTTCTGGAACCGTGGAAATCTCCG	5769
431	QY	CTTGCGCGCTTGGCAGCGCGCTGGGCCCATCTTCCGGAACAGCCCATCGCGCTCATCG	490
5770	Db	CATGCGCTCTTTCGACGAGCTGCTCCGATATTCGGTAACAAACCTCTTTCGGGTGATCG	5829
491	QY	GGCGGGTGATTCCGCGCATGAGGAAAGGCAACTTCTCACCAAGTAGCGATCCCAAGTGT	550
5830	Db	GTGGAGGCGATTACGCAATGGAGAGCAAACTTCTTACAAAATATGGATCCAAAGTGT	5889
551	QY	ACATCATCCACGGGCGCAACACTTCGCGCGCTCCAAAGATTATGCAAGGTAGGGCGCTCT	610
5890	Db	ATATAATCCATTGGAGGGATGCTTTTAGTTCGCTTAAGATTATGCAAGCGCGCGCTTGT	5949
611	QY	CGAATCCTAAGATCCAGGTGTCTGGACTCG-AGTCTGTCAGAGGTATACGGCGGTGCAG	669
5950	Db	CTAATCCTAAGATTGATGTGATTTGGAATCTGCTGTTGTGGAGCTTATGGAGATGGAG	6009
670	QY	CGCGCGGCCCATTAGCTGGGGTCAAGGTCAAGAACTTGTGATGTGTGAGGTGTCTGACC	729
6010	Db	AAAGAGATGTGCTTGAGGAGTGAAGAGTCAAGAAATGTGGTTACCGGTGATGTTCTTGATT	6069
730	QY	TTCAAGTGTCCGGCTTTTCTCGCCATCGGCATGACCGGCCCAAGTTTCTCAATG	789
6070	Db	TAAAGTTTTCTGGATGTTCTTTGCTATTGGTCAATAGCCAGCTACCAAGTTTTGGATG	6129
790	QY	GGCAGCTTCAGCTCCATCGCGATGGGTATGTGCCACCAAGCCGGGCTCTACACATACCA	849
6130	Db	GTGGTGTGAGTTAGATTCCGATGGTTATGTTGTACAGAGCCTGGTACTACACAGACTA	6189
850	QY	GTG-TGGAGGGGTCTTTGTCTGTGGAGACGTGCAGGATTAAGAAGTATCGTCAAGCCATTTA	908
6190	Db	GGCTTCCCGAGTTTTCGCTGGGGTGATGTTTCAGGATTAAGAAGTATAGCAAGCCATCA	6249
909	QY	CTGCTCTGATCAGGTTCATGGCTGCTTTGGACGCCGAGCACTATCTGCAGGAGGTG	968
6250	Db	CTGCTCAGAACTGGTGATGGCAGCTTT-GEATGCAGAGCATTTACTTACAGAGATT	6308
969	QY	GGTGCAAGGTGGCGAAGTCTGATTCA	995
6309	Db	GGATCTCAGCAAGGTAAAGTATTCA	6335

DEC 11 1963

RESULT 13
US-10-290-072-42
; Sequence 42, Application US/10290072
; Publication No. US200302151A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Helffer, Peter

5590 CGATATTTACAGAGCGGTGACGAAAGTCGATTTCTTTCGAAACCGTTAAAGCTATTCA 5649
323 CGGACTCCACACCGTCTCCGCGGACACCGTGTGTCGCGCCACGCGCGCGTTCGCGCGCC 382
5650 CAGATTCGAGGCCATCTCGGTGACGCTGTGATTTCTGCTACTGAGCTGTGGTGAAGC 5709
383 GCCTCCATTTC-----TCCGGTTCGACACCTACTTGGAAACCGCGCATCTCCG 430
5710 GCGTTAGCTTCGTTGGATCGTGGAAGTTCTGGAAGTTCTGGAACCGTGGATCTCCG 5769
431 CTGCGCGCTCTCGACGCGGTGCGCCATCTTCGGAACGAGCCATCGCGGTATCG 490
5770 CATGCGCTGTTGCGACGAGCTCTCCGATATTCGTAACAAACCTCTTCGCGGTGATCG 5829
491 GCGGCGGTGATTCGCGCATGAGGAGGCAACTTCTTCCACCAAGTACGATCCCAAGTGT 550
5830 GTGGAGCGGATTCAGCAATGGAAGGCAACTTCTTACAAATATGATCCCAAGTGT 5889
551 ACATCATTCACCGGCGCACACTTCCGCGCTCCAGATTTATGAGGCTAGGCGGTCT 610
5890 ATATAATCCATTGGAGGAGTGTCTTGTAGTCTTAAGATTTATGAGGCGCGCTTTGT 5949
611 CCAATCTTAAGATCCAGGTGTCTGGGACTCG-AGGTGTCGAGGCTTACGCGGTGCGAG 669
5950 CTAACTTAAGATGATGTGATTTGGAATCTGCTGTGTTGGAAGCTTATGAGATGAG 6009
670 GCGGCGGCCATAGCTGGGGTCAAGGTCAAGAACTTGTGTACTGAGGTGTCTGACC 729
6010 AAAGAGATGTGCTGGAGGATTTGAAAGTGGAAGTGTGTTTACCGGTGATGTTCTGAT 6069
730 TTGAGGTGTCGCGGTCTTCTCGCATCGGCGATGAGCGGCCACCAAGTTTCTCAATG 789
6070 TAAAGTTCTGATGTTCTTCTGCTATTTGCTATGATGAGGCTTACCAAGTTTGGATG 6129
790 GCGAGCTTGAGCTCCATGCGGATGAGGTATGTGGCCACCAAGCGCGGTCTACACATCA 849
6130 GTGGTGTTCGATTTAGATTCGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 6189
850 GTG-TGGAGGGTCTTGTGCTGGAGCTGAGGATAGAGATAGAGATAGAGATAGAGAT 908
6190 GGTTCGCGAGTTTTCGCTGGGGTGTGTTTCAAGATAGAGATAGAGATAGAGATAGAG 6249
909 CTGCTGCTGGATCAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 968
6250 CTGCTGCGAGAACTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6308
969 GTGCGACGCTGGCAGTCTGATTGA 995
6309 GGATCTCAAGAGTGAAGTGAATTGA 6335

RESULT 15

US-10-141-531-42
; Sequence 42, Application US/10141531
; Publication No. US20030100743A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: Del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Luginbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-2/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/141,531
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 208

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 6357
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-10-141-531-42

Query Match 42.8%; Score 425.8; DB 15; Length 6357;
Best Local Similarity 67.4%; Pred. No. 1e-99;
Matches 665; Conservative 0; Mismatches 307; Indels 15; Gaps 4;

QY 23 CGTCCGACGCGCGGTGTGATCATCGGACCGGTCTCTTTCGAGGCTCGATGCGCAACGATCG 82
Db 5350 CTCACAACACAGGCTCTGTATCGTAGAAGTGGCCGACACGCGCGCGCATTT 5409
QY 83 ACGCGGCGCGCGGAGCTCAAGCCGCTCTTTCGAGGCTCGATGCGCAACGATCG 142
Db 5410 ACGCAGTAGGGCTGAACCTTAAACCTCTTCTTCGAGGATGATGCGTAAACGATCG 5469
QY 143 CCGCGGCGCGGAGCTCAACACACGACGCTCGAGAACTTCCCGGATTTCCCAACCG 202
Db 5470 CTCGCGTGTCAACTAACCAACACGACGCTCGAGAACTTCCCGGATTTCCCAAG 5529
QY 203 GCATCATGGGATCGACTCATGACAACTGCGCGCCAGTCCGCTCCGCTCGGACCA 262
Db 5530 GTATTCTCGAGTAGAGCTCATGACAAATTCGTAACAACTCGGAGGATTCGTA 5589
QY 263 ACATCTCTCCGAGACGCTCACCGAGTCAAGTTCTCCGCGCCGCTTCCGCGTCACT 322
Db 5590 CGATATTTCAGAGACGCTGACGAAAGTCAATTTCTTTCGAAACCGTTTAAAGTATCA 5649
QY 323 CCGACTCCACCGCTCTCGCGGACGCTGCTGCGCACGCGCGCGCGCTCGCGCGCC 382
Db 5650 CAGATTCGAGGCTCTCTGCTGAGCTGTGATTTCTGCTACTGAGCTGTGGTGAAGC 5709
QY 383 GCCTCCATTTC-----TCCGGTTCGACACCTACTGGAACCGCGGATCTCCG 430
Db 5710 GCGTTAGCTTCGTTGGATCTGTTGAAAGTTCTGGAAGTTCTGGAACCGTGGATCTCCG 5769
QY 431 CCGCGCGCTCTCGAGGCGCTGCGCCATCTTCGGAACGAGCCATCGCGGTATCG 490
Db 5770 CATGCGCTGTTTTCGAGGAGCTGCTCCGATATTCGTTAACAAACCTCTTTCGCGTATCG 5829
QY 491 GCGCGGTGATTCGCGCATGAGGAGGCAACTTCTTCACCAAGTACGATCCCAAGTGT 550
Db 5830 GTGGAGCGGATTCAGCAATGGAAGGCAAACTTCTTACAAATATGATCCCAAGTGT 5889
QY 551 ACATCATTCGCGGCGCAACCTTCCGCGCTCCAGATTTATGAGGCTAGGCGGTCT 610
Db 5890 ATATAATCCATAGGAGATGCTTTTAGAGCTCTAAGATTTATGAGGCGCGCTTTGT 5949
QY 611 CCAATCTTAAGATCCAGGTGTCTGGGACTCG-AGGTGTCGAGGCTTACGCGGTGCGAG 669
Db 5950 CTAACTTAAGATGATGTGATTTGGAATCTGCTGTGTTGGAAGCTTATGAGATGAG 6009
QY 670 GCGGCGGCCATAGCTGGGGTCAAGGTCAAGAACTTGTGATGCTGAGGTGTCTGACC 729
Db 6010 AAAGAGATGTGCTGGAGGATTCGAAAGTGAAGATGTGTTTACCGGTGATGTTCTGAT 6069
QY 730 TTGAGGTGTCGCGGTCTTCTTCGCGCATGAGCGCGCACCAAGTTTCTCAATG 789
Db 6070 TAAAGTTCTGATGTTCTTCTGCTATTTGCTATGAGGCGGCTACCAAGTTTGGATG 6129
QY 790 GCGAGCTTGAGCTCCATGCGATGGGTATGTGGCCACCAAGCGCGGTCTACACATCA 849
Db 6130 GTGGTGTGAGTTAGATTCGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 6189
QY 850 GTG-TGGAGGGTCTTGTGCTGGAGCTGAGGATAGAGATAGAGATAGAGATAGAGAT 908
Db 6190 GGTTCGCGAGTTTTCGCTGGGGTGTGTTTCAAGATAGAGATAGAGATAGAGATAGAG 6249
QY 909 CTGCTGCTGGATCAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 968

Db 6250 CTGCTGCAGGACTGGGTGCATGCGAGCTTT-GGATGCAGAGCATTACTTACAGAGATT 6308

Qy 969 GGTGCACAGGTGGCAAGTCTGATTGA 995

Db 6309 GGATCTCAGCAAGGTAAAGAGTATTGA 6335

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Job time : 496 secs